

**Placental phenotype and the insulin-like growth factors: resource allocation to fetal growth**

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## ABSTRACT

The placenta is the main determinant of fetal growth and development *in utero*. It supplies all the nutrients and oxygen required for fetal growth and secretes hormones that facilitate maternal allocation of nutrients to the fetus. Furthermore, the placenta responds to nutritional and metabolic signals in the mother by altering its structural and functional phenotype which can lead to changes in maternal resource allocation to the fetus. The molecular mechanisms by which the placenta senses and responds to environmental cues are poorly understood. This review discusses the role of the insulin-like growth factors (IGFs) in controlling placental resource allocation to fetal growth, particularly in response to adverse gestational environments. In particular, it assesses the impact of the IGFs and their signalling machinery on placental morphogenesis, substrate transport and hormone secretion, primarily in the laboratory species, although it draws on data from human and other species where relevant. It also considers the role of the IGFs as environmental signals in linking resource availability, to fetal growth through changes in the morphological and functional phenotype of the placenta. As altered fetal growth is associated with increased perinatal morbidity and mortality and a greater risk of developing adult-onset diseases in later life, understanding the role of IGFs during pregnancy in regulating placental resource allocation to fetal growth is important for identifying the mechanisms underlying the developmental programming of offspring phenotype by suboptimal intrauterine growth.

## KEY POINTS SUMMARY

- Size at birth is critical in determining life expectancy and is dependent primarily on the placental supply of maternal nutrients and oxygen.
- The insulin-like growth factors (IGFs) are important in controlling placental resource allocation to fetal growth during development via their impacts on placental morphogenesis, substrate transport and hormone secretion.
- Placental IGFs (particularly IGF2) alter in response to environmental challenges known to affect placental phenotype and fetal growth.
- IGFs have an important role in optimising fetal growth with respect to resource availability during pregnancy via actions on placental phenotype.

## AUTHOR SUMMARY

Amanda Sferruzzi-Perri received her Bachelor of Science degree with Honours and PhD degree from the University of Adelaide, Australia (in 2001 and 2007, respectively). In 2008, she received a CJ Martin Overseas Biomedical Fellowship from the NH&MRC to undertake research at the University of Cambridge, UK. Through the award of a Next Generation Fellowship from the Centre for Trophoblast Research in 2011 and a Dorothy Hodgkin Research Fellowship from the Royal Society in 2014, Amanda has been using a variety of strategies to decipher the role of insulin-like growth factors and their signalling pathway, PI3K in maternal-placental-fetal interactions governing pregnancy success.

## INTRODUCTION

Intrauterine growth is a key determinant of lifespan. Babies born growth restricted or large for gestational age are at greater risk of perinatal morbidity and mortality than those of normal birth weight. Moreover, the “memories” of an altered environment and growth *in utero* can stretch beyond the perinatal period to influence health much later in life. Epidemiological studies in humans have shown that babies grown abnormally due to poor maternal nutrition are at heightened risk of developing conditions like type 2 diabetes, heart disease and obesity as adults, and of dying younger as a consequence (Gluckman *et al.*, 2005; Jansson & Powell, 2006). Similarly, manipulating intrauterine growth experimentally by varying maternal food intake, dietary composition, oxygen availability, endocrine status or utero-placental blood flow has been shown to program cardiovascular, metabolic and endocrine function of the adult offspring in a wide range of mammalian species (Gluckman *et al.*, 2005; McMillen & Robinson, 2005; Fowden *et al.*, 2006).

As the interface between the mother and fetus, the placenta is one of the main determinants of intrauterine growth. It supplies all the nutrients and oxygen required for fetal growth as well as secreting hormones that influence maternal metabolism in favour of the fetal needs. Its morphological and functional characteristics, therefore, have an important role in determining the allocation of maternal resources to fetal growth. These characteristics include cell composition, surface area, barrier thickness, blood flow, vascularity, nutrient utilisation and the abundance and activity of the various transporter molecules (Fowden *et al.*, 2009; Sandovici *et al.*, 2012). Recent studies have shown that the placenta can respond to maternal nutritional and metabolic signals by altering these characteristics which, in turn, leads to changes in the placental capacity to supply resources to the fetus (Fowden *et al.*, 2009; Sandovici *et al.*, 2012). Thus, the placenta is a key

mediator in linking maternal environmental conditions to development of the fetus (Burton *et al.*, 2016; Sferruzzi-Perri & Camm, 2016). However, the molecular mechanisms by which the placenta senses and responds to environmental cues during pregnancy are poorly understood. This review discusses the role of the insulin-like growth factors (IGFs) in controlling placental resource allocation to intrauterine growth, particularly in relation to maternal environmental conditions during pregnancy. It focuses primarily on small laboratory animals, like mice, rats and guinea pigs that are most commonly used for these studies but also draws on data from other species, including humans, where available.

## THE INSULIN-LIKE GROWTH FACTORS

The insulin-like growth factors (IGFs), IGF1 and IGF2, are 7.5kDa single-chained polypeptides that promote growth, both before and after birth. They affect the metabolism, mitogenesis, survival and differentiation of a wide variety of cell types by binding to IGF receptors (IGF1R and IGF2R), insulin receptor (INSR) and a hybrid IGF1R-INSR receptor with varying affinity (Sferruzzi-Perri *et al.*, 2008; Fernandez & Torres-Aleman, 2012; Harris & Westwood, 2012). Their actions are influenced by at least six different IGF binding proteins (IGFBP-1 to IGFBP-6) and numerous IGF-related binding proteins, which alter access of the IGFs to their receptors and have been reviewed in detail elsewhere (Bach *et al.*, 2005; Bach, 2015; Clemmons, 2016). The main signalling receptor for the IGFs is IGF1R, which activates the phosphoinositide-3 kinase/protein kinase A (PI3K/AKT) and mitogen-activated protein kinase (MAPK) signalling pathways. IGF2 also binds to the IGF2R, which can lead to either IGF2 degradation or activation of the G-protein-coupled signalling pathway (Okamoto *et al.*, 1990).

The *Igf2* gene is subject to parental imprinting and only the paternal allele is expressed. It can be expressed by different promoters, of which P0 (*Igf2P0*) is specific to the placenta in mice (Moore *et al.*, 1997). In mice, though largely not in humans, the *Igf2r* gene is also imprinted but in a reciprocal fashion to *Igf2* with expression from the maternal allele (Monk *et al.*, 2006). The IGFs (particularly IGF2), their receptors and signalling pathways are expressed by the placenta in many species and change in their abundance both developmentally and in response to environmental cues (Sferruzzi-Perri *et al.*, 2010). In many species, circulating IGF concentrations are higher during pregnancy than in the non-pregnant animal and also change in the mother and fetus with proximity to delivery (Fowden, 2003; Sferruzzi-Perri *et al.*, 2010). IGF2 is more abundant than IGF1 in both the maternal

and fetal circulations in all species studied to date, with the exception of mice (Fowden, 2003; Sferruzzi-Perri *et al.*, 2010). IGF2 is also more highly expressed than IGF1 by the placenta in all species studied to date (Sferruzzi-Perri *et al.*, 2010).

## THE EFFECTS OF THE INSULIN-LIKE GROWTH FACTORS ON PLACENTAL PHENOTYPE

The effects of the IGFs on the placenta have been studied directly in two main ways. First, they have been given exogenously either to placental cultures *in vitro* or to pregnant animals *in vivo* to study placental growth, transport and endocrine function. Secondly, the *Igf* genes, their receptors and key molecules in their downstream pathways have been under- or over-expressed in genetically modified mice to determine the morphological and functional consequences for the placenta at different stages of pregnancy. While the functions of the placenta are common across species, its structure varies in terms of shape, organisation of trophoblast lineages, extent of invasion into the maternal uterus, and degree of interdigitation at the feto-maternal interface (reviewed in depth elsewhere (Carter, 2007; Wooding & Burton, 2008; Roberts *et al.*, 2016)). For instance, the human and non-human primate placenta is composed of a series of highly branched structures, called villi. These contain a mesenchymal core that has fetal capillaries which are closely associated with an overlying syncytiotrophoblast layer. The syncytiotrophoblast is directly bathed in maternal blood and functions in both transport and hormone secretion. Cytotrophoblast cells, can fuse to form the syncytiotrophoblast or migrate from the villous tree into the decidua where they invade and remodel uterine spiral arteries to promote blood flow to the placenta. The syncytiotrophoblast is also bathed in maternal blood in the mouse, rat and guinea pig placenta. However, the mouse placenta is arranged into two morphologically and functionally distinct regions; the labyrinth zone (Lz) that is responsible primarily for transport and the junctional zone (Jz; also known as basal or interlobium region) which functions in uterine remodelling/invasion and hormone secretion. In ruminant species like the sheep and cow the placenta is comprised of individual placentomes which form at specialised sites called caruncles, in the uterine wall. The overlying trophoblast layer can be a syncytium (in sheep) or remains uni-cellular (columnar epithelium; in cows) and there is no invasion of the maternal blood vessels by trophoblast cells. However, in sheep some trophoblast cells migrate and fuse with caruncle epithelial cells and play an endocrine role.

## Exogenous administration of IGFs

### ***In vitro experiments***

IGF1 and IGF2 prevent apoptosis and enhance proliferation and migration/invasion of human placental villous explants, primary trophoblast cultures and trophoblast cell lines from the first trimester and term (Table 1). IGF1 also promotes the proliferation, invasion and survival of first trimester human placental fibroblasts (Miller *et al.*, 2005) and the differentiation of term trophoblast cells into syncytiotrophoblast (Bhaumick *et al.*, 1992; Milio *et al.*, 1994; Cohran *et al.*, 1996). Similarly, IGF1 stimulates proliferation and migration of murine ectoplacental cone trophoblast in culture (Kanai-Azuma *et al.*, 1993) and early pregnancy porcine trophoblast cells (Jeong *et al.*, 2014). Furthermore, IGF2 promotes differentiation of murine ectoplacental cone trophoblast and migration of ovine trophoblast cells *in vitro* (Kim *et al.*, 2008). Using receptor and pathway inhibitors and IGF analogues with selectivity for particular receptors, some of the molecular mechanisms mediating the actions of IGFs on the human placenta have begun to be identified *in vitro*. IGFs appear to mediate their proliferative and anti-apoptotic effects on trophoblast through activating IGF1R and triggering the MAPK and PI3K/AKT signalling pathways, respectively (Forbes *et al.*, 2008). IGFs also induce trophoblast migration and invasion through IGF1R, and possibly INSR with subsequent activation of MAPK and PI3K/AKT signalling pathways (Diaz *et al.*, 2007; Shields *et al.*, 2007; Forbes *et al.*, 2008; Mayama *et al.*, 2013). However, IGF2 may also signal via IGF2R and G<sub>i</sub> proteins, MAPK and Rho GTPase pathways to trigger trophoblast migration and invasion (McKinnon *et al.*, 2001; Shields *et al.*, 2007; Harris *et al.*, 2011). Thus IGFs promote the growth of different cell lineages in the placenta via multiple mechanisms (Figure 1A).

In addition to stimulating placental growth, both IGFs stimulate glucose and System A amino acid uptake and IGF1 increases System L activity but reduces lipoprotein lipase activity in human trophoblast *in vitro* (Table 1). However, these changes in nutrient uptake do not always track with the expression of the transporter genes or proteins, suggesting that the IGFs may also affect post-transcriptional/translational mechanisms (Fang *et al.*, 2006; Jones *et al.*, 2013; Jones *et al.*, 2014). Indeed, IGF1 was recently shown to stimulate glucose transporter capacity by increasing the translocation of GLUT1/SLC2A1 to the trophoblast plasma membrane (Baumann *et al.*, 2014). In culture, IGF1 prevents the release of the vaso-constrictors, prostaglandin E and F, and thromboxane, by the term human placenta and reduces the agonist-mediated vasoconstriction of human myometrial arteries (Siler-Khodr *et al.*, 1995; Corcoran *et al.*, 2012). *In vivo*, these effects could increase utero-placental blood flow and substrate transfer in late gestation. Both IGF1 and IGF2 also enhance trophoblast endocrine capacity in culture. IGFs increase the secretion of hormones including progesterone, human chorionic gonadotrophin and placental lactogen *in vitro* although

others, like placental growth hormone may not be affected (Maruo *et al.*, 1995; Zeck *et al.*, 2008; Rak-Mardyla & Gregoraszczuk, 2010). In addition, IGF2 simulates the differentiation of hormone-producing murine and ovine trophoblast *in vitro* (Kanai-Azuma *et al.*, 1993; Kim *et al.*, 2008). Thus, IGFs have the capacity to promote growth, hormone secretion and substrate transport capacity of the placenta.

### ***In vivo experiments***

Treatment of guinea pig dams with either IGF1 or IGF2 in early-mid pregnancy increases fetal weight near term [Table 1; (Sferruzzi-Perri *et al.*, 2006)]. With exogenous IGF1, placental Lz area and *Igf2* gene expression is reduced during the treatment, even though fetal weight is increased already in mid pregnancy (Sohlstrom *et al.*, 2001; Sferruzzi-Perri *et al.*, 2007b; Standen *et al.*, 2015). Whilst there is no sustained effect of either IGF on placental weight, IGF2 increases the volume and surface area of the transport Lz, near term [Table 1, (Sferruzzi-Perri *et al.*, 2006)]. Development of the placental exchange region was further enhanced when the IGF2R-selective synthetic analogue, Leu<sup>27</sup>-IGF2 was administered maternally (Sferruzzi-Perri *et al.*, 2008). In mice, maternal Leu<sup>27</sup>-IGF2 treatment from day 13 of pregnancy halves the number of fetuses naturally growth-restricted within the litter near term (Charnock *et al.*, 2016). Taken together, these findings suggest that maternal IGF2 in early gestation may act, in part, via the IGF2R to enhance functional development of the placenta with beneficial impacts on fetal growth. However, caution is warranted as part of the effects of Leu<sup>27</sup>-IGF2 could be due to the displacement of endogenous IGF2 and its subsequent interaction with IGF1R and INSR in the placenta.

Exogenous IGFs also modify the functional capacity of the placenta to supply resources for fetal growth. In the late pregnant ewe, increasing IGF1 in the fetal circulation increases amino acid and glucose uptake by the placenta but may reduce materno-fetal transfer of these substrates, lactate production and the number of placentomes (Table 1). Increasing IGF1 in the maternal circulation also alters placental metabolic function in the pregnant ewe near term; glucose transfer capacity and lactate production are enhanced by an acute infusion of IGF1 (Liu *et al.*, 1994). In guinea pigs, placental delivery of glucose and/or neutral amino acids to the fetus is increased in late gestation by chronic maternal IGF treatment in early-mid pregnancy (Table 1). This enhanced placental transfer in late gestation is partly due to increased expression of nutrient transporters (System A amino acid; *SNAT2/Slc38a2*) by IGF1 in mid pregnancy and improved development of the exchange region by IGF2 in late pregnancy (Sferruzzi-Perri *et al.*, 2006; Sferruzzi-Perri *et al.*, 2007b). In mice, the

variability in System A amino acid transport capacity and conceptus weight within the litter is abolished by maternal Leu<sup>27</sup>-IGF2 (Charnock *et al.*, 2016) and data suggest that IGFs may have most benefit for improving growth of the smallest pups. Indeed, maternal Leu<sup>27</sup>-IGF2 improves the weight of fetuses that are growth restricted due to a lack of the endothelial nitric oxide gene and reduces the number of pups below the fifth centile of the wild-type population in late gestation (Charnock *et al.*, 2016). In addition to improving placental transport function, exogenous IGFs also affect endocrine capacity *in vivo* (Figure 1B). Maternal IGF2 treatment simulates the development of the endocrine Jz of the rat placenta (Van Mieghem *et al.*, 2009) and exogenous IGF1 and IGF2 increase placental pro-renin activation in guinea pigs (Standen *et al.*, 2015). Thus, IGFs may also increase fetal resource supply through changing placental endocrine function and thus maternal adaptations to pregnancy, however further studies are warranted.

To circumvent possible confounding effects of systemic IGF treatment on the mother, approaches are being developed to target IGFs to the placenta. In mice, adenoviral-mediated site-specific intraplacental transfer of the *Igf1* gene on day 14 of pregnancy, increases the area of the placenta, the size of the Lz and of the maternal and fetal facing areas three days later, although there is no change in conceptus weight [Table 1; (Katz *et al.*, 2009)]. In response to liposome-mediated targeting of IGF2 to the mouse placenta, placental growth is also increased although fetal weight is not affected (King *et al.*, 2016). In rabbits, the weight of natural runt fetuses in the litter is increased two days following placental *Igf1* transgene delivery without a change in placental weight however how it impacts on structure and function of the placenta remains unknown (Keswani *et al.*, 2015). These data suggest that targeting of IGF delivery to the placenta may prove an effective method of improving placental function and, thus, fetal growth, particularly when feto-placental growth is impaired.

### **Genetic manipulation of the IGF system**

In mice, knockout of the *Igf2* gene in the entire conceptus or predominantly within the fetal or trophoblast cell lineages leads to placental and fetal growth restriction, with the greatest reduction in growth seen with ubiquitous *Igf2* loss (Table 2). Similarly, a heterozygous deficiency in the PI3K-p110 $\alpha$  (*Pik3ca*; homozygous deficiency is lethal) or complete ablation of the AKT1 (*Pkba*) or MAPK1 (*Erk2*) genes, causes feto-placental growth restriction (Cho *et al.*, 2001; Hatano *et al.*, 2003; Yang *et al.*, 2003; Yung *et al.*, 2008; Kent *et al.*, 2012; Sferruzzi-Perri *et al.*, 2016). In contrast, over-expressing the *Igf2* gene through activating the normally silent maternal gene copy in the *H19* null, increasing



IGF2 availability via *Igf2r* ablation, or deletion of the PI3K signalling inhibitor (*Pten*), results in overgrowth of the fetus and placenta (Leighton *et al.*, 1995; Ludwig *et al.*, 1996; Louvi *et al.*, 1997; Ripoche *et al.*, 1997; Church *et al.*, 2012). Deletion of the *Igf1*, *Igf1r* or *Insr* genes in mice also leads to fetal growth restriction, but placental weight is unaffected (DeChiara *et al.*, 1990; Baker *et al.*, 1993; Louvi *et al.*, 1997). This suggests that the growth-promoting effect of IGF2 in the mouse placenta occurs independently of IGF1R and INSR, possibly through an unknown, distinct placental-specific receptor (XRp) (Louvi *et al.*, 1997). However, evidence from *H19* null mutants suggests that IGF1R could contribute to the control of placental growth in mice as the first exon of the *H19* gene encodes *miR-675* which targets *Igf1r* for reduced expression (Keniry *et al.*, 2012). Overgrowth of the *H19* null placenta (Leighton *et al.*, 1995; Esquiliano *et al.*, 2009; Angiolini *et al.*, 2011; Church *et al.*, 2012), is thus thought to be due to biallelic *Igf2* via imprinting mechanisms, as well as, enhanced *Igf1r* expression through loss of *miR-675* (Keniry *et al.*, 2012). Taken together, these data highlight the importance and complexity of the IGF system in controlling conceptus growth in mice.

Genetic manipulations of *Igf2*, *Igf2r* and the downstream signalling pathways also affect the morphology of the placenta (Table 2). For instance, loss of *Igf2* (complete and *Igf2P0* null), *Pik3ca*, *Pkba* or *Erk2* gene expression causes defective Lz formation. In particular, Lz volume/thickness, exchange surface area and vascularisation are all reduced and the interhaemal barrier to diffusion of gases like oxygen is greater in the placenta of all these mutants (Table 2). In contrast, in the *H19* null, the Lz surface area is increased in line with the placentomegally observed (Angiolini *et al.*, 2011). In addition, IGF2 affects the formation of endocrine cells in the placenta. In particular, loss or gain of *Igf2* or the PI3K-AKT signalling pathway causes a disproportionate decrease or expansion of the glycogen cells in the Jz, whereas *Igf1r* or *Insr* nulls show no changes in Jz glycogen cell abundance (Table 2). Collectively, the available data suggest that IGF2 acts via both the PI3K/AKT and MAPK pathways to attain normal placental weight and Lz structure, and through PI3K/AKT signalling to drive placental glycogen cell formation in mice (Figure 2A).

Placental function also changes when the IGF system is genetically modified in mice (Table 2). The passive permeability of the placenta to hydrophilic nutrients/solutes is reduced in the complete *Igf2* null, placental-specific *Igf2P0* null and *H19* null (Constancia *et al.*, 2002; Sibley *et al.*, 2004; Coan *et al.*, 2008b; Angiolini *et al.*, 2011). The complete *Igf2* null placenta transports less neutral amino acid (methyl amino-isobutyric acid, MeAIB) via the System A transporters in association with reduced *SNAT2/Slc38a2* expression (Constancia *et al.*, 2005). There is also reduced abundance of System X<sub>AG</sub><sup>-</sup> and System Y<sup>+</sup> transporters, responsible for placental transfer of cationic and anionic amino acids, in

the complete *Igf2* and the *Igf1r* null (Matthews *et al.*, 1999). In contrast, the *Igf2P0* null placenta transports more neutral amino acids via System A, as well as, more glucose and calcium in late gestation (Table 2). Up-regulation of placental transport capacity is associated with increased expression of *SNAT4/Slc38a4* and *GLUT3/Slc2a3* by the *Igf2P0* deficient placenta. In contrast to *Igf2*, there is little or no information on the capacity of the *Igf1* or *Insr* null placenta to supply nutrients to the fetus. In the complete *Igf2* null, placental and fetal growth restriction occurs concurrently and becomes evident in mid-gestation [Table 2; (Baker *et al.*, 1993; Constancia *et al.*, 2005)]. In the *Igf2P0* null, placental weight is reduced at a similar time in gestation, but fetal growth only becomes restricted much closer to term and to a lesser extent than in the complete *Igf2* null (Baker *et al.*, 1993; Constancia *et al.*, 2002; Constancia *et al.*, 2005). Liposome-mediated targeting of IGF2 to the placenta has recently been shown to increase the weight of *Igf2P0* null mouse fetuses near term [Table 1; (King *et al.*, 2016)]. Collectively, these findings suggest that the *Igf2P0* null placenta compensates for its defective development and compromised permeability by adaptively up-regulating its nutrient transport systems and thereby, minimises the degree of fetal growth restriction, relative to the complete *Igf2* null. The *Pik3ca* heterozygote deficient placenta also transfers glucose and amino acids via System A transporters with increased efficiency in compensation for its impaired development, which is associated a less severe reduction in fetal weight close to term than earlier in gestation (Sferruzzi-Perri *et al.*, 2016). Moreover, the naturally small placenta that supports more fetal mass per gram shows increased expression of *Igf2P0* coupled with a preservation of Lz growth and with increased placental System A transport capacity and *SNAT2/Slc38a2* abundance compared to the large placenta in the litter (Coan *et al.*, 2008a). In contrast, the over-grown *H19* null placenta shows diminished neutral amino acid and glucose transport which is thought to limit fetal over-growth and avoid an excessive drain of maternal resources into the fetus (Angiolini *et al.*, 2011). Thus, IGF2 in the placenta is important for fine-tuning nutrient supply to the fetus (Figure 2B).

In addition to effects on placental transport, the *Igf2* gene may also affect the endocrine function of the placenta with consequences for maternal physiology during pregnancy. Evidence for this stems from associations between altered placental Jz formation in *H19* and *Igf2P0* null mutants and raised circulating glucose, insulin and/or corticosterone in phenotypically wild-type dams (Petry *et al.*, 2010; Sferruzzi-Perri *et al.*, 2011). Thus, IGF2 has an important role in nutrient allocation to the fetus. By regulating placental phenotype, it balances the fetal genetic drive for growth with the maternal ability to supply the required resources, thereby optimising both offspring and maternal fitness.

## IGFS AS ENVIRONMENTAL SIGNALS IN REGULATING PLACENTAL RESOURCE ALLOCATION TO FETAL GROWTH

IGFs may also play an important role in changing placental resource allocation to the fetus in environmentally-challenged pregnancies. As *Igf1* expression is relatively low in the placenta, studies have largely focussed on placental expression of *Igf2* and activation of its signalling pathways (Table 3). However, since the signalling pathways are responsive to both IGFs, the placenta can also respond to changes in circulating IGF1 and IGF2 induced by nutritional or other environmental cues.

### Maternal nutrition

#### *Undernutrition*

In mice, guinea pigs and baboons, undernutrition restricts placental growth in association with a decrease in the expression of *Igf2* and/or signalling via the PI3K/AKT and MAPK pathways (Table 3). There are also reductions in placental vascularisation, exchange surface area, Jz volume and glycogen cell abundance and/or a greater barrier to diffusion with maternal undernutrition in mice and guinea pigs; morphological parameters that were altered similarly by a genetic deficiency in *Igf2*, *Pik3ca*, *Pkb* and *Erk2* (Tables 2 and 3). Together, these studies suggest that decreases in IGF2 expression and signalling within the placenta could underlie the growth and morphological defects observed with maternal undernutrition in these species. In larger animals, the expression of *Igf2* and its signalling machinery reduces, is unchanged or even increases in response to undernutrition (Table 3). For instance, signalling via MAPK and PI3K/AKT in the placenta is up-regulated in nutrient-restricted ewes and hiefers (Zhu *et al.*, 2007a; Zhu *et al.*, 2007b; Ma *et al.*, 2011). In these models, changes in signalling relate to a normalisation of placental weight or an increase in placental cotyledon vascularity. They also correlate with a maintenance or restoration of fetal weight in later gestation, despite an exposure to undernutrition. In ewes of a moderate condition, which have the smallest placentas supporting more mass of fetus per gram, placental expression of *Igf2* is greatest (Osgerby *et al.*, 2003). These studies therefore suggest that in larger species, there is morphological adaptation of the placental to an adverse maternal nutritional state through increasing *Igf2* and growth signalling locally.

In the undernourished sheep placenta with increased PI3K/AKT and MAPK signalling, the expression of glucose and fatty acid transporters is also increased (Ma *et al.*, 2011). However, in undernourished baboons, diminished *Igf2* expression and signalling in the placenta accompanies reductions in System A and L amino acid transporter capacity and glucose transporter gene expression (Pantham *et al.*, 2015; Pantham *et al.*, 2016). Taken together, these studies suggest that IGF2 and the PI3K/AKT and MAPK signalling pathways could also mediate changes in placental transport function during undernutrition. In mice, despite a 20% reduction in maternal food intake and placental growth restriction earlier in gestation, fetal weight is normal until just prior to term (Coan *et al.*, 2010). This maintenance of fetal growth relates to an initial preservation of Lz development in earlier gestation and an adaptive up-regulation of System A amino acid transporter capacity and *SNAT2/Slc38a2* expression near term, by the growth restricted undernourished placenta. However, in mice lacking the placental-specific *Igf2* isoform (*Igf2P0*) these adaptations to maternal undernutrition fail to occur. The development of the placental exchange region is compromised earlier in gestation, there is no up-regulation of amino acid transport or *SNAT2/Slc38a2* expression and reduced *SNAT4/Slc38a4* abundance near term in *Igf2P0* null placentas compared to wildtype in undernourished mice (Sferruzzi-Perri *et al.*, 2011). As a result, fetal growth is restricted earlier in gestation and more adversely affected near term by undernutrition, in *Igf2P0* nulls. The *Igf2P0* transcript is, therefore, a major determinant of the environmental modification of placental phenotype with undernutrition in mice. The expression of genes involved in glucose, neutral amino acid and fatty acid transport, as well as, the IGF signalling pathways in the human placenta are modified by the diet and physical activity of the mother during pregnancy (Brett *et al.*, 2015). Thus, the IGF system may also be important for modifying resource capacity of the human placenta in response to changes in the maternal environment.

### ***Low-protein diets***

During rodent pregnancy, consumption of an iso-caloric low protein diet has inconsistent impacts on both placental weight and placental *Igf2* expression [Table 3 and (Sferruzzi-Perri & Camm, 2016)]. However, the nature of the specific effect appears to depend on the degree of protein deprivation, stage of pregnancy studied and sex of the conceptus (Jansson *et al.*, 2006; Coan *et al.*, 2011; Nusken *et al.*, 2011; Gao *et al.*, 2012a). Despite the contrasting results, placental *Igf2* expression seems to track positively with the weight of the placenta in mice and rats (Coan *et al.*, 2011; Nusken *et al.*, 2011; Gao *et al.*, 2012a). For instance, in pregnant mice, low protein diets cause placentomegaly and the degree of placental weight increase relates to the level of *Igf2* up-regulation at first appearance

of growth enhancement (Coan *et al.*, 2011). The variation in placental growth and *Igf2* expression observed in different models of protein deficiency could be caused by the content and source of carbohydrate used to maintain calorie intake. Nevertheless, taken together, these findings suggest that at least part of the changes in placental growth seen with protein deprivation could be mediated through local changes in *Igf2*.

There are also changes in placental transport capacity with gestational protein malnutrition. For instance, in response to a diet with 8% protein, the mouse placenta adaptively transports more glucose to the fetus on day 16 of pregnancy (Coan *et al.*, 2011). This up-regulation occurs when placental *Igf2* expression is also increased and when fetal growth is maintained despite maternal protein deprivation (Coan *et al.*, 2011). A few days later however, glucose transport is unchanged, System A amino acid transporter abundance is reduced and *Igf2* expression no longer increased in the placenta by a low protein diet, and fetal growth restriction ensues (Coan *et al.*, 2011). These data suggest that placental *Igf2* may be important for adapting nutrient supply to the fetus in response to maternal protein malnutrition in mice. However, there is evidence that pathways downstream of *Igf2* may also be important. For instance, the mechanistic target of rapamycin (mTORC1) mediates the mitogenic and metabolic actions of IGFs (Jansson *et al.*, 2012b). In rats, protein deprivation reduces mTORC1 signalling, Systems A and L amino acid transport and *SNAT2/Slc38a2*, *LAT1/Slc7a5* and *LAT2/Slc7a8* expression by the placenta, prior to the appearance of placental and fetal growth restriction (Jansson *et al.*, 2006; Rosario *et al.*, 2011). These findings suggest that down-regulation of signalling pathways like mTORC1 and amino acid transporters in the placenta could link maternal protein restriction to decreases in fetal growth. The availability of protein and specific amino acids during pre-implantation rodent development is linked to alterations in the expression of genes within the *H19-Igf2* locus, mTORC1 signalling and trophoblast cell formation and differentiation with consequences for feto-placental phenotype in late gestation (Kwong *et al.*, 2006; Van Winkle *et al.*, 2006; Eckert *et al.*, 2012; Watkins *et al.*, 2015). Thus, changes in *Igf2* expression and its signalling pathways could be responsive to the availability of nutrients from the earliest stages of development.

### ***Diets with excess sugar and/or fat***

The expression of *Igf2* and its signalling pathways in the placenta are inconsistently altered by diets with excess sugar and/or fat (Table 3). Weight of the conceptus may also be reduced, increased or unchanged, depending on the level of fat in the diet, the amount of simple sugars consumed and the

timing of the dietary manipulation [Table 3 and reviewed in (Sferruzzi-Perri & Camm, 2016)]. Part of these variations in *Igf2* expression and conceptus growth could be due to the differences in protein and micronutrient intake, as species like mice and rats control their calorie intake tightly (Keesey & Hirvonen, 1997). In mice fed a diet containing 2.5-times the fat of the controls, placental weight is reduced in early pregnancy in association with decreases in the expression of *Igf2* and signalling machinery, including *Mtor* (Sasson *et al.*, 2015). These placental changes accompanied reductions in the expression of System A amino acid transporter, *SNAT1/Slc38a1*, glucose transporter *GLUT1/Slc2a1* and/or fatty acid translocase, *CD36* depending on the length of high fat feeding and whether the diet was eaten before pregnancy (Sasson *et al.*, 2015). In over-nourished ewes, placental weight is reduced in mid-gestation in association with decreased activity of the IGF signalling pathway (including activation of IRS1 and mTORC1) and changes in vessel size and density in the placenta (Zhu *et al.*, 2009; Ma *et al.*, 2010). However, fetal weight is increased along with fatty acid transporters and translocases in the placenta, suggesting that alternative signalling pathways may be activated to adapt placental nutrient supply to the fetus in ewes with excess food intake (Zhu *et al.*, 2010; Tuersunjiang *et al.*, 2013).

In other studies, increases in the placental IGF system are coupled with improved placental resource allocation to the fetus in dams fed obesogenic diets (King *et al.*, 2013; Sferruzzi-Perri *et al.*, 2013; Diaz *et al.*, 2015; Rosario *et al.*, 2015; Rosario *et al.*, 2016). For instance, in mice, consumption of a high sugar and fat diet from day 1 of pregnancy initially causes conceptus growth restriction and morphological defects in the placental Lz. However, fetal weight normalises by term, despite the persistence of placental growth and morphological defects through adaptive up-regulation of glucose and neutral amino acid transport to the fetus by the placenta (Sferruzzi-Perri *et al.*, 2013). Up-regulation of transport capacity relates to increased expression of *GLUT3/Slc2a3* and *SNAT2/Slc38a2*, as well as, elevated expression of the placental-specific *Igf2* isoform and PI3K/AKT signalling in the placenta in dams fed a diet with excess sugar and fat. Obesogenic diets fed from before pregnancy also increase placental nutrient transporter capacity (glucose, Systems A and L amino acid and fatty acids) in line with greater *Igf2* or PI3K/AKT and mTORC1 signalling, however responses varied with the precise composition of the diet and possibly, fetal sex (King *et al.*, 2013; Aye *et al.*, 2015; Diaz *et al.*, 2015; Rosario *et al.*, 2015; Rosario *et al.*, 2016). The expression of IGF signalling machinery (receptors, AKT, mTORC1) and nutrient transporters is also altered in the placenta from obese women, however, the specific nature of these changes appears to depend on the level of maternal body fat mass, gestational weight gain and whether macrosomia is observed (Jansson *et al.*, 2012a; Brett *et al.*, 2016; Martino *et al.*, 2016). Taken together, these findings suggest

that obesity and obesogenic diets alter placental phenotype in association with changes in placental *Igf2* system and fetal growth.

### **Maternal hypoxia**

In mice, hypoxia typically reduces fetal growth in a severity-dependent manner without a change in placental weight [Table 3 and reviewed in (Sferruzzi-Perri & Camm, 2016)]. However, if the hypoxic challenge commences early in pregnancy, placentomegaly is observed in association with greater maternal blood spaces and activation of the PI3K/AKT and mTORC1 signalling pathways in the placenta (Matheson *et al.*, 2015). Even though placental weight may not be altered when maternal hypoxia commenced later in pregnancy, placental expression of the IGF system and capacity to supply resources to the fetus is altered (Table 3). In particular, placental expression of IGF receptors, INSR and PI3K isoforms is decreased in response to five days of 13%-10% maternal hypoxia in late mouse gestation, and in 10% hypoxia this effect is due to reductions in maternal food intake (Cuffe *et al.*, 2014; Higgins *et al.*, 2015). However, expression of *Igf2*, *Igf2P0* and activated AKT increases with 13% hypoxia, but is unchanged or even decreased in response to 5 days of 12-10% hypoxia near term (Cuffe *et al.*, 2014; Higgins *et al.*, 2015). In the 13% hypoxic mouse placenta showing increases in IGF2 expression and signalling, there are beneficial changes in Lz structure including improved vascularisation, maternal blood spaces and a thinner diffusion barrier to exchange; changes that would optimise oxygen delivery to the fetus near term (Higgins *et al.*, 2015; Matheson *et al.*, 2015). There is also greater placental glucose uptake and transport and maintained delivery of neutral amino acids to the fetus when 13% hypoxia occurs in the last third of pregnancy (Higgins *et al.*, 2015). In contrast, in the 12-10% hypoxic placenta with unchanged or decreased expression of the IGF2 system, the morphology of the placental Lz is compromised, with reductions in maternal blood spaces and surface area and a greater barrier to diffusion; changes that would further limit fetal oxygen supply in hypoxic dams (Cuffe *et al.*, 2014; Higgins *et al.*, 2015). Moreover, placental glucose uptake and transport capacity is not up-regulated or even reduced (less *GLUT1/Slc2a1*) and delivery of neutral amino acids diminished, in dams exposed to 12-10% hypoxia, depending on whether food intake is reduced and the sex of the fetus (Cuffe *et al.*, 2014; Higgins *et al.*, 2015). In culture, 1% hypoxia reduces the outgrowth of mouse ectoplacental cone trophoblast in association with diminished *Igf2* expression (Pringle *et al.*, 2007). Hypoxia (1% oxygen) also diminishes the expression of PI3K/AKT and mTORC1 signalling in human trophoblast cell lines (Yung *et al.*, 2012a) and modulates IGF1 and IGF2 signalling in early pregnancy placental mesenchymal stem cells (Youssef *et al.*, 2014; Youssef & Han, 2016). Placental expression of the PI3K/AKT and mTORC1 signalling

pathways and *GLUT1/Slc2a1* expression are decreased in women at 3100m above sea level who deliver growth-restricted babies (Zamudio *et al.*, 2006; Yung *et al.*, 2012a). In addition, inducing endoplasmic stress in the mouse placental Jz genetically is associated with defects in PI3K/AKT and mTORC1 signalling, altered IGF2 glycosylation and bioactivity, and with feto-placental growth restriction (Yung *et al.*, 2012b). Taken together, these findings suggest that activating IGF2 and/or PI3K/AKT signalling in the placenta may be critical for adapting placental resource allocation to the fetus during hypoxia in late pregnancy. They also suggest that the placenta may integrate signals of oxygen and nutrient availability through the IGF2 system to adapt its phenotype and optimize maternal resource supply to fetal growth. Indeed, the mouse *Igf2* gene harbours a hypoxia-responsive element in its promoter (Feldser *et al.*, 1999), as well as CHORE motifs, which bind the glucose-responsive transcription factor, MLX (Hunt *et al.*, 2015). Therefore, the availability of oxygen and nutrients *in utero* could have direct effects on placental *Igf2*. Nutritional and hypoxic challenges alter the concentration of hormones like the glucocorticoid stress hormone and insulin, in the maternal circulation (Sferruzzi-Perri *et al.*, 2011; Cuffe *et al.*, 2014). Thus, changes in placental phenotype may reflect alterations in the metabolic and endocrine state of the mother.

### **Maternal endocrine challenges**

Endocrine challenges can affect maternal metabolism and utilisation of nutrients and thus the partitioning of resource to the conceptus in pregnancy (Vaughan *et al.*, 2011). Administering corticosterone or the synthetic glucocorticoid, dexamethasone to rodents for 3-7 days reduces fetal and placental weights during gestation [Table 3 and (Vaughan *et al.*, 2011)]. In mice, corticosterone decreases AKT and mTORC1 activation in association with reductions in feto-placental weight, Lz vascularisation and glucose and System A amino acid transporter capacity, however the specific nature of these effects depend on when in pregnancy the over-exposure occurs (Table 3). Administering the synthetic glucocorticoid, dexamethasone reduces the expression of MAPK and weight of placenta in female, but not male conceptuses and there is no change in glucose and *SNAT/Slc38a* amino acid transporters irrespective of fetal sex (Cuffe *et al.*, 2011). In mice, placental *Igf2* expression is unaffected by maternal administration of corticosterone and dexamethasone even though the conceptus may be growth-restricted (Cuffe *et al.*, 2011; Vaughan *et al.*, 2012; Vaughan *et al.*, 2015). Whereas restrain stress increases placental *Igf2* but does not alter offspring weight in mice (Pankevich *et al.*, 2009). In rats, dexamethasone decreases placental *Igf2* and the level of activated AKT, particularly in the endocrine Jz (Ain *et al.*, 2005). In dexamethasone-treated rats, there are reductions in the expression of prolactin-related family genes by the Jz in late gestation, which may influence the maternal adaptations to pregnancy and, thus, alter the fetal supply of



nutrients indirectly (Ain *et al.*, 2005). The expression of *Igf2* by the term human placenta is also altered in women with elevated plasma cortisol during pregnancy due to emotional distress (Mina *et al.*, 2015). Glucocorticoid response elements have been identified in the human *Igf1* gene promoter (He *et al.*, 2016) however, very little is known about whether glucocorticoids could have direct effects on placental *Igf2* expression. Collectively these findings suggest that reductions in placental *Igf2* system and the functional phenotype of the placenta could link elevated maternal glucocorticoids to decreases in fetal growth.

In rats, pre-existing maternal diabetes also alters the expression of the IGF system in the placenta, as well as, materno-fetal resource allocation, however, the direction of change depends on how long the dam was insulin deficient/dysglycemic. For instance, *Igf* expression and IGF1R activation are elevated in association with greater glycerol and free fatty acid transfer by the placenta and an increase in fetal weight by 13% in rats that are diabetic from neonatal life (White *et al.*, 2015). Placental lipid transport capacity is also increased in rat dams that are diabetic for 1 week prior to pregnancy (increase in placental lipoprotein lipase), however, the expression of *Igf2* and the IGF signalling machinery is decreased and the abundance of *GLUT1/Slc2a1* reduced in association with a more minor increase in fetal weight (by 5%) (Cisse *et al.*, 2013). Genetically-inducing maternal insulin insensitivity by a global heterozygous deficiency in PI3K-p110 $\alpha$  signalling capacity in the mouse dam is associated with improved placental Lz development (larger surface area and thinner barrier to diffusion), but reduced glucose transport and expression of nutrient (*GLUT1/Slc2a1*, *SNAT1/Slc38a1*, *SNAT2/Slc38a2*) and prolactin-related family genes near term (Sferruzzi-Perri *et al.*, 2016). However, the specific nature of these placental changes depended on whether the conceptus itself was heterozygous for the PI3K-p110 $\alpha$  deficiency (Sferruzzi-Perri *et al.*, 2016). Moreover, there is no effect of maternal heterozygous deficiency in PI3K-p110 $\alpha$  signalling on fetal weight in this model, irrespective of fetal genotype (Sferruzzi-Perri *et al.*, 2016). Taken together, these studies suggest that the IGF2/PI3K-p110 $\alpha$  system plays an important role in modulating fetal nutrition and growth in response to maternal insulin deficiency and/or insensitivity, by acting at the level of placental transport phenotype.

#### ***Other environmental challenges affecting conceptus growth***

The expression of *Igfs*, receptors and signalling machinery in the placenta also changes in response to insults that affect the placental capacity to supply the fetus with nutrients. Such insults include reduced utero-placental blood flow, heat stress and alcohol consumption (Table 3). Reducing both

maternal oxygen and nutrient supply to the conceptus using uterine artery ligation in mice, rats and guinea pigs, or placental embolism in sheep, reduces placental expression of components of the IGF system in association with defects in placental Lz structure and in transporter expression and activity of the glucose and Systems A and L amino acid transporters (Table 3). The extent of these changes however, depends on timing of the insult in the pregnancy. In sheep, removal of uterine caruncles prior to pregnancy is associated with increased placental *Igf2* expression and an adaptive increase in placentome size, trophoblast and maternal capillary volume and surface area, although total placental mass and fetal weight, are reduced [Table 3; (Zhang *et al.*, 2016b)]. Acute exogenous IGF1 does not alter nutrient metabolism by the embolised sheep placenta [Table 1; (Jensen *et al.*, 1999)]. However, several doses of intra-amniotic IGF1 increases glucose and Systems A and L amino acid transporter expression by the embolised placenta and improves feto-placental growth *in vivo* [Table 1; (Eremia *et al.*, 2007; Wali *et al.*, 2012)]. Moreover, in mice with uterine artery ligation, targeting of IGF1 to the placenta using a nanoparticle or adenoviral-mediated approach increases the abundance of glucose and Systems A and L amino acid transporters in the placenta, placental width and fetal growth [Table 1; (Jones *et al.*, 2013; Jones *et al.*, 2014; Abd Ellah *et al.*, 2015)]. These findings highlight the therapeutic potential of IGFs for improving the capacity of the placenta to supply nutrients to the fetus in compromised pregnancies.

In ewes, heat stress reduces placental growth and glucose transport capacity, as well as, alters the expression of IGF1 and IGF2, and AKT, mTORC1 and MAPK signalling pathways during gestation (Table 3). In rats, alcohol consumption during the peri-conceptual period leads to late gestational fetal growth restriction but no change in placental weight (Gardebjer *et al.*, 2014). However, Lz development and *Igf1*, *Igf1r* and *SNAT2/Slc38a2* expression is decreased, but Jz glycogen cell formation, *Igf2* and GLUT1/Slc2a1 may be increased in response to peri-conceptual alcohol exposure near term (Gardebjer *et al.*, 2014). This suggests there can be programmed changes in the conceptus leading to changes in the IGF system and the structural and functional phenotype of the placenta that link the maternal environment from the earliest stages of pregnancy to fetal growth near term.

## CONCLUSIONS AND PERSPECTIVES

Thus, IGFs are important regulators of placental resource allocation to fetal growth both developmentally and in response to environmental manipulations known to program the ill health of offspring. They increase placental morphogenesis, substrate transport and hormone secretion,

which, in turn promotes fetal growth either directly via the supply of nutrients and oxygen or indirectly via the maternal metabolic adaptation to pregnancy and the availability of nutrients for transplacental transport. In response to environmental challenges, the IGFs (particularly IGF2) and their signalling pathways change in line with the alterations in placental structure and function, and thereby, link changes in the maternal environment to fetal substrate supply and growth during pregnancy with implications for developmental programming. The environmentally-induced changes in the IGF system and placental phenotype may be beneficial (obesogenic diets, moderate hypoxia) or detrimental (eg. severe oxygen and nutrient deprivation and glucocorticoid excess) to resource allocation to the fetus depending on the type, severity and timing of the challenge during pregnancy (Figure 3). The beneficial effects of IGF treatments on placental phenotype show promising therapeutic potential for improving fetal growth in situations in which placental growth is impaired without major maternal compromise, particularly when the treatment with IGF1 or IGF2 is targeted directly to the placenta. However, efforts to understand the regulation of endogenous placental IGF expression may also be fruitful, particularly in the case of *Igf2* which appears to be most important for mediating adaptive responses locally in mice. These findings are important in the context of human pregnancy as dysregulated expression of the IGFs and signalling components are often reported in the human placenta associated with abnormal fetal growth (Abu-Amero *et al.*, 1998; Sheikh *et al.*, 2001; Gratton *et al.*, 2002; Gurel *et al.*, 2003; Laviola *et al.*, 2005; Scioscia *et al.*, 2006; Street *et al.*, 2006; Trollmann *et al.*, 2007; Akram *et al.*, 2008; Yung *et al.*, 2008; Colomiere *et al.*, 2009; Borzsonyi *et al.*, 2011; Street *et al.*, 2011; Demendi *et al.*, 2012; Jansson *et al.*, 2012a; Iniguez *et al.*, 2014; Nawathe *et al.*, 2016; Zhang *et al.*, 2016a). However, it is important to note, that several causes of environmental, maternal, and fetal origin, can lead to changes in placental phenotype and fetal growth in humans (Gaccioli & Lager, 2016). Thus studies of animal models showing alterations in the expression of IGFs and their signalling pathways provides insight but further information is required on the natural conditions of variable placental phenotype among humans.

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**Abstract figure. The proposed actions of IGFs on placental resource allocation to drive fetal growth.** Note that changes in placental IGFs and resource allocation depend on the timing and severity of the environmental insult.

**Figure 1. Impact of exogenous IGFs on the placenta.** **A)** The effect of exogenous IGFs on placental human trophoblast *in vitro*. Proposed signalling pathways mediating the actions of IGFs shown. **B)** The effect of exogenous maternal IGFs on the mouse, rat and/or guinea pig placenta *in vivo*. Dashed lines indicate a potential interaction (A) or impact (B) of IGF1. IGF = insulin-like growth factor, IGF1R = type 1 IGF receptor, IGF2R = type 2 IGF receptor, INSR = insulin receptor, Jz = junctional zone, Lz = labyrinthine zone, MAPK = mitogen-activated protein kinase, PI3K = phosphoinositol 3-kinase.

**Figure 2. The effect of genetically manipulating IGF2 expression or signalling on placental phenotype in mice.** **A)** shows the effect of complete loss of IGF2 and **B)** shows the effect of partial loss of IGF2, either by deleting the placental-exclusive isoform, *Igf2P0* or through a constitutive heterozygous deficiency of PI3K-p110 $\alpha$ . Dashed line indicates a potential interaction of IGF2 with receptor. Line with a round head indicates parameters reduced by loss of IGF2 signalling. Loss of IGF2 signalling leads to reductions in placental development and transport function (A). Partial loss of IGF2 signalling also leads to reductions in placental development, but is associated with adaptive up-regulation in transport function (B). AA = amino acids, IGF = insulin-like growth factor, IGF1R = type 1 IGF receptor, Lz = labyrinthine zone, MAPK = mitogen-activated protein kinase, PI3K = phosphoinositol 3-kinase, XRp = unknown placental-specific IGF receptor.

**Figure 3. The effect of different environmental manipulations on the placental IGF system and resource allocation phenotype in the mouse.** **A)** shows manipulations which down-regulate IGF2

signalling. **B)** shows manipulations which up-regulate IGF2 signalling. AKT = protein kinase B, IGF = insulin-like growth factor, Lz = labyrinthine zone. \* Note *Igf2P0* is required for the placenta to up-regulate amino acid transport to the fetus in response to maternal undernutrition.



1532 **Table 1.** The impact of exogenous IGF1 or IGF2 on the placental phenotype and fetal outcome (where available)

IGF	System	Species	Treatment	Study	Placental size and morphology	Placental function	Fetal weight	References
IGF1	<i>In vitro</i>	Mouse	Primary ectoplacental cone trophoblast	First trimester	↑ proliferation and migration			(Kanai-Azuma <i>et al.</i> , 1993)
		Pig	Primary trophoblast cells	First trimester	↑ proliferation and migration			(Jeong <i>et al.</i> , 2014)
		Human	1 <sup>st</sup> trimester primary trophoblast	First trimester	↑ invasion via INSR and IGF1R activation of Akt			(Mayama <i>et al.</i> , 2013)
		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ proliferation and syncytial formation via IGF1R-mediated MAPK signalling, ↓ apoptosis via IGF1R-mediated PI3K signalling			(Forbes <i>et al.</i> , 2008; Forbes <i>et al.</i> , 2015)
		Human	1 <sup>st</sup> trimester placental trophoblast	First trimester	↑ proliferation, migration			(Hashimoto <i>et al.</i> , 2010)
		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ proliferation			(Forbes <i>et al.</i> , 2009; Forbes <i>et al.</i> , 2015)
		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ migration			(Lacey <i>et al.</i> , 2002)

		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ proliferation	↑hCG, hPL		(Maruo <i>et al.</i> , 1995)
		Human	1 <sup>st</sup> trimester trophoblast	First trimester		↑System A amino acid and glucose uptake		(Kniss <i>et al.</i> , 1994)
		Human	1 <sup>st</sup> trimester primary placental fibroblasts	First trimester	↑proliferation, invasion, ↓ apoptosis			(Miller <i>et al.</i> , 2005)  *Ad-IGF-I
		Human	BeWo syncytial cell line		↑ proliferation, invasion, ↓ apoptosis	↑ System A and System L amino acid transporter activity, Snat1, Snat2, Lat1, 4F2hc, GLUT1, GLUT3 and GLUT8, ↓Lat2		(Jones <i>et al.</i> , 2013; Jones <i>et al.</i> , 2014)  *Ad-hIGF-I
		Human	BeWo			↔ pGH		(Zeck <i>et al.</i> , 2008)
		Human	JEG-3 choriocarcinoma cell line		↑proliferation, ↓apoptosis	↑ P4, hCG secretion		(Rak-Mardyla & Gregoraszczuk, 2010)
		Human	JEG-3		↑invasion via induction of adhesion and migration through IGF1R-PI3K and MAPK signalling			(Diaz <i>et al.</i> , 2007)
		Human	BeWo			↑ System A amino acid transporter activity via PI3K signalling, ↔ Snat1 or		(Fang <i>et al.</i> , 2006)

						Snat2		
		Human	BeWo, term explants and term perfused human placenta			↑ glucose transport, GLUT1 membrane abundance		(Baumann <i>et al.</i> , 2014)
		human	Term human placenta	Term		↓ LPL activity in		(Magnusson-Olsson <i>et al.</i> , 2006)
		Human	Term trophoblast	Term		↑ System A amino acid uptake		(Bloxam <i>et al.</i> , 1994; Karl, 1995; Yu <i>et al.</i> , 1998)
		Human	Term trophoblast and cell lines	Term	↑ syncytialisation			(Bhaumick <i>et al.</i> , 1992; Milio <i>et al.</i> , 1994; Cohran <i>et al.</i> , 1996)
<b>IGF2</b>	<i>In vitro</i>	Mouse	Primary ectoplacental cone trophoblast	First trimester	↑ differentiation into endocrine cells			(Kanai-Azuma <i>et al.</i> , 1993)
		Sheep	Primary trophoblast	First trimester	↑ migration			(Kim <i>et al.</i> , 2008)
		Human	1 <sup>st</sup> trimester HTR8_SVneo cell line	First trimester	↑ migration via Rho GTPases			(Qiu <i>et al.</i> , 2005; Shields <i>et al.</i> , 2007)
		Human	1 <sup>st</sup> trimester HTR8_SVneo cell line	First trimester	↑ migration via signalling through IGF2R involving inhibitory G proteins and the MAPK pathway			(McKinnon <i>et al.</i> , 2001)

		Human	1 <sup>st</sup> trimester primary trophoblast	First trimester	↑ migration/invasion			(Irving & Lala, 1995; Hamilton <i>et al.</i> , 1998)
		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ trophoblast proliferation and syncytial formation via IGF1R-mediated MAPK signalling, ↓ apoptosis via IGF1R-mediated PI3K signalling			(Forbes <i>et al.</i> , 2008; Forbes <i>et al.</i> , 2009; Forbes <i>et al.</i> , 2015)
		Human	JEG-3 choriocarcinoma cell line		↑ invasion via induction of adhesion and migration through INSR-PI3K and MAPK signalling			(Diaz <i>et al.</i> , 2007)
		Human	SGHPL4 and 1 <sup>st</sup> trimester villous explants	First trimester	↑ proliferation, migration and invasion			(Pollheimer <i>et al.</i> , 2011)
		Human	1 <sup>st</sup> trimester primary placental fibroblasts	First trimester	↑ proliferation and invasion, ↓ apoptosis			(Miller <i>et al.</i> , 2005) *Ad-IGF-II
		Human	1 <sup>st</sup> trimester and term trophoblast	First trimester	↓ apoptosis, ↑ proliferation and survival against TNF- $\alpha$ and IFN- $\gamma$ -induced apoptosis			(Hills <i>et al.</i> , 2012)
		Human	1 <sup>st</sup> trimester placental	First		↑ glucose uptake		(Kniss <i>et al.</i> , 1994)

			trophoblast	trimester				
		Human	1 <sup>st</sup> trimester placental trophoblast	First trimester		↑ glucose and System A amino acid uptake		(Kniss <i>et al.</i> , 1994)
		Human	1 <sup>st</sup> trimester placental explant	First trimester	↑ migration			(Lacey <i>et al.</i> , 2002)
		Human	In BeWo and term explants		↑ proliferation ↓ apoptosis and necrosis			(Harris <i>et al.</i> , 2011)
IGF1	<i>In vivo</i>	Mouse	D14	D17	↔ weight, ↑ placental cross-sectional area, Lz and fetal and maternal facing areas		↔ weight or viability	(Katz <i>et al.</i> , 2009)  * Ad-hIGF-I
		Mouse uterine artery ligation	D16	D20	↔ weight, ↑ placental thickness		↑27%, ↔ fetal viability	(Abd Ellah <i>et al.</i> , 2015)  * nanoparticle targeted delivery to placenta: PLAC1-hIGF-1
		Mouse uterine artery ligation	D18	D20	ND	↑4F2hc, Lat1, Lat2, GLUT8, GLUT9a/b, ↔ Snat1, Snat2,	ND	(Jones <i>et al.</i> , 2013; Jones <i>et al.</i> , 2014)

						GLUT1		* Ad-hIGF-I
		Guinea pig	D20-37	D40	↔ weight		↑ 6%, ↓ litter size	(Sohlstrom <i>et al.</i> , 2001)
		Guinea pig	D20-38	D35	↑ 17% weight, ↓ placental and Lz area, ↔ Lz, Jz, FC, MBS, Troph Vd	↑ glucose and System A amino acid transfer, Snat2 and prorenin activation, ↓ Igf2, ↔ Glut1, Igf1	↑ 15%	(Sferruzzi-Perri <i>et al.</i> , 2007b; Standen <i>et al.</i> , 2015)
		Guinea pig	D20-38	D62	↔ weight ↔ structure	↑ glucose and System A amino acid transfer	↑ 17% ↑ fetal viability	(Sferruzzi-Perri <i>et al.</i> , 2006; Sferruzzi-Perri <i>et al.</i> , 2007a)
		Guinea pig 30%UN	D20-37	D40	↑ 13% weight		↔	(Sohlstrom <i>et al.</i> , 2001)
		Rabbit  Natural runt in litter	D19	D21	↔ weight		↑ 19%	(Keswani <i>et al.</i> , 2015)  * Ad-hIGF-I

		Sheep	D128, 4hr infusion	D128	ND	↑ glucose transfer and lactate production, ↔ blood flow, urea or glucose transfer	ND	(Liu <i>et al.</i> , 1994)
		Sheep * Fetal infusion	D121-132	D132	↔ weight, ↓ placentome number	↓ glucose and System A amino acid transfer	↔	(Bloomfield <i>et al.</i> , 2002b)
		Sheep * Fetal infusion	D128, 4hr infusion	D128	ND	↓ glucose transfer, lactate uptake and umbilical flow, ↔ urea transfer or serine uptake	ND	(Harding <i>et al.</i> , 1994; Jensen <i>et al.</i> , 1999; Jensen <i>et al.</i> , 2000)
		Sheep Embolised * Fetal infusion	D128, 4hr infusion	D128	ND	↔ glucose or urea transfer, lactate uptake and umbilical flow	ND	(Jensen <i>et al.</i> , 1999)
		Sheep Spontaneous growth restriction * Fetal infusion	D128, 4hr infusion	D128	ND	↔ glucose or urea transfer, lactate uptake and umbilical flow	ND	(Jensen <i>et al.</i> , 1999)
		Sheep Embolised * Intra-	D110, D117, D124	D120-131	↔ but placentas no longer significantly different to untreated controls	↔ glucose uptake, ↑ Glut1, Glut4, Systems y+ and L transporters (Slc7a1 and	↔ weight, ↑ fetal growth rate and fetuses no longer significantly different	(Eremia <i>et al.</i> , 2007; Wali <i>et al.</i> , 2012)

		amniotic infusion				Slc7a8) ↔ Glut3, Snat4, Slc7a5	to untreated controls	
<b>IGF2</b>	<i>In vivo</i>	Mouse	D14, D16, D18  IGF2 (1mg/kg/day) or iRGD-liposome with IGF2 (0.3mg/kg/day)	D18	↑ weight		↔	(King <i>et al.</i> , 2016)
		Mouse IGF2P0	D14, D16, D18  treatment with iRGD- liposome with IGF2 (0.3mg/kg/day)	D18	↔ weight of Igf2P0 and WT		↑ Igf2P0 but not WT	(King <i>et al.</i> , 2016)
		Rat	D16-22	D22	↔ weight, ↑ Jz		↔	(Van Miegheem <i>et al.</i> , 2009)
		Guinea pig	D20-37	D40	↑ 9% weight		↑ 7%	(Sohlstrom <i>et al.</i> , 2001)
		Guinea pig	D20-38	D35	↔ weight and structure	↔ glucose or System A amino acid transfer, Glut1, Snat2, Igf1 and Igf2, ↑prorenin activation	↔	(Sferruzzi-Perri <i>et al.</i> , 2007b; Standen <i>et al.</i> , 2015)
		Guinea pig	D20-38	D62	↔ weight, ↑ Lz area, Vd, Vol, SA, ↓ Jz Vd, ↔ BT	↑ glucose transfer, ↔ System A amino acid transfer	↑ 11% weight and ↑ fetal viability	(Sferruzzi-Perri <i>et al.</i> , 2006; Sferruzzi-Perri <i>et al.</i> , 2007a)



		Guinea pig 30%UN	D20-37	D40	↔ weight		↔	(Sohlstrom <i>et al.</i> , 2001)
<b>Leu<sup>-</sup><sub>27</sub></b> <b>IGF-II</b>	<i>In vivo</i>	Mouse	D13-19	D19	↔ weight	↔ System A amino acid transfer, ↓ litter System A amino acid variability	↔ weight, ↓ variability in fetal weight	(Charnock <i>et al.</i> , 2016)
		Mouse  eNOS-/-	D13-19	D19	↔ weight		↑	(Charnock <i>et al.</i> , 2016)
		Guinea pig	D20-38	D62	↔ weight, ↑ Lz vd, Troph, MBS Vd and Vol and SA, ↓ Jz area, Vd, Vol, FC Vd, Vol and BT	↑ glucose and System A transfer and prorenin activation	↑ 11%	(Sferruzzi-Perri <i>et al.</i> , 2008)

1533 For *in vivo* studies, exogenous IGF was administered to the mother, unless stated otherwise. Abbreviations: BT=barrier thickness, D=day, FC=fetal capillaries, GLUT=glucose transporter,  
1534 hCG=human chorionic gonadotrophin, hPL=human placental lactogen, IGF1/Igf1=insulin-like growth factor-1, IGF2/Igf2=insulin-like growth factor-2, Jz=junctional zone, LAT=cationic amino  
1535 acid transporter, Lz=labyrinthine zone, MAPK/ERK=mitogen activated kinase, MBS=maternal blood space, ND=not determined; P4=progesterone; PI3K=phosphoinositol 3-kinase,  
1536 pGH=placental growth hormone, Prl=prolactin-related hormone, SA=surface area, SNAT/Slc38a= Sodium-coupled neutral amino acid transporter, vol=volume, vd=volume density.

1537 **Search terms used:** trophoblast, placenta, fetus, insulin-like growth factor, IGF and/or transport

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1539 Table 2. The effect of genetically manipulating IGF abundance and/or signalling on feto-placental growth in mice

Manipulation	Approach	Placental			Fetal weight	Reference
		size	morphology	function		
Deficiency of IGF and downstream signalling						
Global IGF1 KO	Igf1-/-	D18/19 ↔			D18/19 ↓40%	(Baker <i>et al.</i> , 1993)
Global IGF2 KO	Paternal Igf2-	D15 ↓47%  D18/19 ↓20-30%	D15 ↓ Jz GlyT  D18/19 ↔ Lz and Jz Vd ↓ Jz GlyT	D17 ↓ EAAT1, EAAT2 (Jz), EAAT3 (Jz), EAAT4,↑ CAT1, ↔ 4f2hc  D18/19 ND	D15 ND  D18/19 ↓40% ↑ fetal loss	(DeChiara <i>et al.</i> , 1990; DeChiara <i>et al.</i> , 1991; Baker <i>et al.</i> , 1993; Liu <i>et al.</i> , 1993; Lopez <i>et al.</i> , 1996; Matthews <i>et al.</i> , 1999; Esquiliano <i>et al.</i> , 2009; Church <i>et al.</i> , 2012; Kent <i>et al.</i> , 2012)
Global IGF2 KO	Paternal transmission LacZDMR2–	D16 ↓27%  D19 ↓40%	D16 ND  D19 ↓ Lz vd and volume of all Lz components, SA, FC length and diffusing capacity, ↑ Jz vd and BT	D16 ↔ System A and glucose transport, Snat1, Snat2, Snat4  D19 ↓ System A transfer and passive permeability and Snat2, ↔ glucose transport, Snat1 and Snat4	D16 ↓24%  D19 ↓52%	(Constancia <i>et al.</i> , 2005; Coan <i>et al.</i> , 2008b)
Fetal specific IGF2 KO	Inner cell mass Igf2-	D17 ↓14%			D17 ↓27%	(Gardner <i>et al.</i> , 1999)
Placental trophoblast specific IGF2 KO	Trophechoderm Igf2-	D17 ↓21%			D17 ↓12%	(Gardner <i>et al.</i> , 1999)
Placental Lz specific	Paternal transmission	D16 ↓20%	D16 ↔ Lz or Jz Vd	D16 ↑ System A and	D16 ↔/↓4%	(Constancia <i>et al.</i> , 2002;

IGF2 KO	Igf2P0-	D17 ↓24%  D19 ↓35%	↓ Lz Trophoblast, GlyT  D19 ↓ SA, trophoblast, FC volume, FC length, diffusing capacity, ↑ BT ↔ Lz or Jz vd and umbilical artery flow	glucose transport, Snat4, Glut3, ↓ passive permeability, calbindin, ↔ Snat1, Snat2, Glut1  D19 ↑/↔ System A transport, ↑glucose and calcium transport, ↓ passive permeability, ↔ Snat1, Snat2, Snat4, calcium transport, calbindin, PMCA1, TRPV6	D17 ↓24%  D19 ↓24%	Sibley <i>et al.</i> , 2004; Constancia <i>et al.</i> , 2005; Coan <i>et al.</i> , 2008b; Dilworth <i>et al.</i> , 2010; Kusinski <i>et al.</i> , 2011; Sferruzzi-Perri <i>et al.</i> , 2011; Dilworth <i>et al.</i> , 2013)
Global IGF1R KO	Igf1r-	D19 ↔	D18/19 ↔ Jz GlyT	D17 ↓ EAAT2 (Jz), EAAT3 (Lz and Jz), ↑ CAT1, ↔ EAAT1, EAAT4	D19 ↓55%	(DeChiara <i>et al.</i> , 1990; Louvi <i>et al.</i> , 1997; Matthews <i>et al.</i> , 1999) (Esquiliano <i>et al.</i> , 2009)
Global INSR KO	INSR-	D15 ↔ D18/19 ↔	D15 ↔ Jz GlyT D18/19 ↔ Jz GlyT		D15 ND D18/19 ↓10%	(Louvi <i>et al.</i> , 1997; Esquiliano <i>et al.</i> , 2009)
PI3K p110α (Pik3ca)	Kinase dead heterozygote Pik3ca-D933A	D16 ↓9%	D16 ↓Lz vol, FC vol, FC length, MBS vol, SA, diffusing capacity, ↑ BT, ↔ Jz	D16 ↑ glucose and System A transfer per unit SA, ↔ Glut1, Glut3, Snat1, Snat2, Snat4	D16 ↓19%	(Sferruzzi-Perri <i>et al.</i> , 2016)

		D19 ↓12%	D19 ↓ Lz vol, FC vol, FC length, Troph vol, SA, diffusing capacity, ↑ BT, ↔ Jz	D19 ↑ glucose and System A transfer per unit SA, ↑ Prl3b1, ↔ Glut1, Glut3, Snat1, Snat2, Snat4	D19 ↓11%	
Global decreased AKT signalling through increased PTEN	Prl2-/-	D17 ↓22%	D17 ↓Jz, GlyT and Lz	D17 ↓ passive transport	D17 ↓17%	(Dong <i>et al.</i> , 2012)
Global decreased AKT1 signalling	Pkba-/- (exons 4-8 deleted)	D17 ↓33%  D19 ↓45%	D17 ↓ thickness, GlyT, Lz vessel density, length, area	D17 ↓ pAkt  D19 ↓ total Akt, pAkt ↑ Akt2 and Akt3	D17 ↓17%	(Yang <i>et al.</i> , 2003; Yung <i>et al.</i> , 2008)
Global decreased AKT1 signalling	Pkba-/- (exon 1 deleted)	D18 ↓30%	D18 ↔ Lz and Jz Vd	D18 ↓ pAkt, ↔ p-Akt	D18 ↓22% weight and ↑ fetal loss	(Cho <i>et al.</i> , 2001; Kent <i>et al.</i> , 2012)
Global decreased MAPK signalling	Erk2-/-	D11 ↓	D11 ↓ Lz thickness, FC development	↓ MAPK signalling	D11 ↓ weight and ↑ fetal loss	(Hatano <i>et al.</i> , 2003)
<b>Over-expression of IGF and downstream signalling</b>						
Global IGF2 over-expression	Maternal Igf2r-	D16 ↑40% D18 ↑25%			D16 ↑40% D18 ↑40%	(Ludwig <i>et al.</i> , 1996; Louvi <i>et al.</i> , 1997)
Global IGF2 over-expression*	Maternal H19Δ13-	D15 ↑37%  D16 ↑30%	D15 ↑ Jz GlyT  D16 ↑ volume of all placental components, ↑ SA, diffusing capacity, ↔BT	D15 ↑ Akt1 ↔ pAkt, p-ERK1/2 D16 ↓ glucose transfer, passive permeability and Glut3, ↔Glut1, Snat1, Snat2, Snat4	D15 ↑30%  D16 ↑12%	(Leighton <i>et al.</i> , 1995; Esquiliano <i>et al.</i> , 2009; Angiolini <i>et al.</i> , 2011; Church <i>et al.</i> , 2012)

		D18 ↑60%	D18 ↑Jz GlyT		D18 ↑20%	
		D19 ↑45%	D19 ↑ volume of all placental components, SA, diffusing capacity	D19 ↓ glucose and System A transfer, passive permeability and Snat4, ↔ Glut1, Glut3, Snat1, Snat2	D19 ↑23%	
Global increased IGF2 and signalling via AKT	Double KO of maternal H19 and Pten +/-	D16 ↑65% D19 ↑80%	D16 ↑ Jz, GlyT D19 ↑ Jz, GlyT	↑ p-AKT and IGF2	D16 ↑31% D19 ↑31%	(Church <i>et al.</i> , 2012)
Global increased pAKT	Pten +/-	D16 ↑22% D19 ↑22%	D16 ↑ Jz, GlyT D19 ↑ Jz, GlyT	↑ p-AKT, ↔ IGF2	D16 ↑19% D19 ↑7%	(Church <i>et al.</i> , 2012)

1540 \*H19 null has biallelic expression of Igf2 combined with absence miR675 (encoded by H19)

1541 Abbreviations: BT=barrier thickness, D=day, FC=fetal capillaries, GLUT/Slc2a=glucose transporter, GlyT=trophoblast glycogen cells, IGF1/Igf1 =insulin-like growth factor-1, IGF2/Igf2=insulin-  
1542 like growth factor-2, Jz=junctional zone, LAT=L-type amino acid transporter, Lz=labyrinthine zone, MBS=maternal blood space, ND=not determined, PI3K=phosphoinositol 3-kinase, SA=surface  
1543 area, SNAT/Slc38a= Sodium-coupled neutral amino acid transporter, Vd=volume density.

1544 **Search terms used:** placenta, fetus, insulin-like growth factor, IGF, PI3K, ERK, MAPK, knock out, deficiency and/or transgenic

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1547 Table 3. The effect of maternal environmental challenge on fetal growth and placental structure, function and IGF signalling.

Maternal manipulation	Species	Timing	Placental				Fetal weight	Reference
			IGF and signalling	size	morphology	function		
<b>Nutrient restriction</b>								
20% UN	Mouse	D3-D19	D16 ↑ IGF1R ↓ Igf2P0 and PI3K signalling D19 ↓ Igf2P0 and PI3K signalling	D16 ↓6%  D19 ↓9%	D16 ↔Lz but ↓Jz and GlyT  D19 ↓Lz (MBS and FC vols and SA), ↔BT	D16 ↓ Glut1  D19 ↑ System A amino acid transport, ↑ Glut1, Snat2, ↓Snat4	D16 ↔  D19 ↓13%	(Coan <i>et al.</i> , 2010; Sferruzzi-Perri <i>et al.</i> , 2011)
10-30% UN	Guinea pig	-D28	D35/40 ↓Igf2, ↔ Igf1	D35 ↓20%  D60 ↓30%	D35 ↓ Jz volume ↔ Lz, but ↓ MBS, SA and ↑ BT  D60: ↓ Lz volume, MBS, FC, SA, ↑ BT, ↔ Jz,		D35 ↓29%  D60 ↓35%	(Roberts <i>et al.</i> , 2001; Olausson & Sohlstrom, 2003)
30% UN	Sheep	D22-D135	D135 ↔ Igf2	D135 ↓19% , altered placentome distribution			D135 ↓12%	(Osgerby <i>et al.</i> , 2002, 2004)
50% UN	Sheep	-D60-D30	D78 ↑ Insulin-IGF signalling (p-Akt and p-	D78 ↓29%	D78 ↑ vascularity		D78 ↔	(Zhu <i>et al.</i> , 2007b)

			ERK1/2)					
50% UN	Sheep	D28-D78	D78 ↑ Insulin-IGF signalling (p-ERK1/2, ↔pAkt) ↔ mTORC1 signalling D135 ↔	D78 ↓21%  D135 ↔		D78 ↑ Glut3, GLUT1, Fatp4  D135 ↑ Fatp4	D78 ↓26%  D135 ↔	(Ma <i>et al.</i> , 2011)
UN gradual decrease to full food withdrawal	Sheep	D83-D90	D90 ↔ Igf2  D135 ↓Igf2	D90 ↓22%  D135 ↔		D90 ↔ Glut1, Glut3 D135 ↔ Glut1, Glut3	D90 ↔  D135 ↔	(McMullen <i>et al.</i> , 2005)
UN 50%	Cow	D30-D125	D125 ↑ Insulin-IGF signalling (p-Akt and p-ERK1/2) D250 ↔	D125 ↓27%  D250 ↓20%	D125 ↑ vascularity  D250 ↔ vascularity		D125 ↔  D250 ↔	(Zhu <i>et al.</i> , 2007a)
70% UN	Baboons	D30-D165	D90 ↓ Igf2, IGF2R, ↑ IGF1R, ↔ Igf1 or IGF1 D120 ND	D90 ↔  D120 ↔		D90 ND  D120 ↓ System A amino acid transport, ↔ system L amino acid transport, GLUT1 TAUT, SNAT1, SNAT2, SNAT4, LAT1,	D90 ↔  D120 ↔	(Li <i>et al.</i> , 2007; Pantham <i>et al.</i> , 2015) (Kavitha <i>et al.</i> , 2014)

			D165 ↓ insulin/IGF-I, MAPK (IRS-1, Akt S6K, ERK-1) and mTOR signalling	D165 ↓20%		LAT2 D165 ↓ System A and L amino acid transport, GLUT1, TAUT, SNAT2, LAT1, LAT 2	D165 ↓19%	
<b>Low protein diets</b>								
16% v 20% protein (0.80CT)	Mouse	D3-19	D16 ↔ Igf2, H19  D19 ↔ Igf2, H19	D16 ↑5%  D19 ↑5%	D16 ↓ Lz/Jz ratio  D19 ↓ Lz/Jz ratio	D16 ↑ glucose transport, Glut1, ↔ System A amino acid transport  D19 ↓ System A amino acid transport, Snat4, ↔ glucose transport,	D16 ↔  D19 ↔	(Coan <i>et al.</i> , 2011)
8% vs 20% protein (0.40CT)	Mouse	D3-19	D16 ↑ total Igf2 ↔ Igf2P0, H19	D16 ↔	D16 ↔	D16 ↑ glucose transport, Snat2, ↔ System A amino acid	D16 ↔	(Coan <i>et al.</i> , 2011)



			D19 ↔ Igf2, H19	D19 ↑4%	D19 ↔	transport D19 ↓ Snat1, Snat4, ↔ glucose and System A amino acid transport	D19 ↓9%	
9% vs 17% protein (0.53CT)	Rat	D1-22	D22 ↑Igf1 ↓Igf2 ↔Igf1r,Igf2r,Insr	ND			D22 ↓8%	(Nusken <i>et al.</i> , 2011)
6% vs 20% protein (0.30CT)	Rat	D1-21	D14 ↓ Lz Igf2, Insr in female and ↑ Lz IGF2, ↓ Igf1r in male  D16 ↓ Lz Igf2 in female and male D21 ↓ Lz IGF2 in male and female	D14 ↓25% D18 ↓12%    D21 ↔	D14 ↓Lz and Jz vol D18 ↓Lz vol, ↑ trophoblast stem cells and Lz sinuosoidal GiT, ↓ spongiotrophoblast and GiT cells, ↔Jz D21↔Lz ↓Jz		D14 ↓21.5 D18 ↓27    D21 ↓14%	(Gao <i>et al.</i> , 2012a; Gao <i>et al.</i> , 2012b, 2013)
4% vs 18% protein (0.22CT)	Rat	D2-21	D19 and D21 ↓ mTOR  D21 ↓ PI3K signalling (p-Akt-T308)	D15-19 ↔  D21 ↓12.5%	ND	D19 and D21 ↓ Systems A and L amino acid transport, LAT1, LAT2, SNAT2, ↔ glucose transport,	D15-19 ↔  D21 ↓21%	(Jansson <i>et al.</i> , 2006{Rosario, 2011 #3227; Pantham <i>et al.</i> , 2016)

						SNAT4		
<b>Obesogenic diets</b>								
2.5-times fat	Mouse	-D28-D1	D13 ↓ Igf2, Mtor, ↔ Igf1  D18 ↓ Igf2, Igf2r, ↔ Igf1	D13 ↓ 20%  D18 ↑ 15% in males, ↔ females	↔ Lz	D13 ↓ Snat1, Glut1, ↔ Cd36  D18 ↓ Cd36, ↔ Snat1, Glut1	D13 ↓ 28%  D18 ↓ 15%	(Sasson <i>et al.</i> , 2015)
2.5-times fat	Mouse	-D28-D18	D1 ↑ 3 Igf1r, ↓ Igf2, Igf2r, Mtor, ↔ Igf1  D18 ↓ Igf2, Igf2r, ↔ Igf1	D13 ↓ 20% in males  D18 ↔ males or females	↔ Lz	D13 ↓ Snat1, Glut1, ↔ Cd36  D18 ↓ Cd36, ↔ Snat1, Glut1	D13 ↓ 25%  D18 ↓ 25%	(Sasson <i>et al.</i> , 2015)
2.5-times fat	Mouse	D1-D18	D13 ↑ Igf1r, ↓ Igf2, Igf2r, Mtor, ↔ Igf1  D18 ↓ Igf2, Igf2r ↔ Igf1	D13 ↓ 20% in males  D18 ↑ 15% in males	↔ Lz	D13 ↓ Snat1, Glut1, Cd36  D18 ↓ Glut1, Cd36 ↔ Snat1	D13 ↓ 28%  D18 ↓ 28%	(Sasson <i>et al.</i> , 2015)
5.3-times fat	Mouse	-D84-D19	D15 ↑ Igf2 and Igf2r male, ↔ female  D19 ↔ Igf2 and Igf2r	D15 ↔  D19 ↔		D15 ↑ Lz Snat2 in male, ↑ Lz Snat4 in female  D19 ↔	D15 ↔  D19 ↓ 8% in males	(King <i>et al.</i> , 2013)
6-times fat	Mouse	D1-15	D15 ↑ Igf1, ↓ Irs1 in	D15 ↑ 7%	D15 ↔ Lz or	D15 ↓ Slc22a1,	D15 ↔	(Gallou-Kabani <i>et al.</i> ,

			males, ↔ Igf2, Igf2P0, Igf2r, H19		vascularity	↑ Slc22a2 *sexually dimorphic response of placenta		2010; Gabory <i>et al.</i> , 2012)
2.5-times fat	Rat	D1-D21	D21 ↔ mTORC1 signalling	D21 ↔	D21 ↓ Jz		D21 ↓5%	(Mark <i>et al.</i> , 2011)
5-6-times fat	Rat	-D49-D21	D21 ↑ mTORC1 signalling, ↔ Insulin-IGF signalling (p-Akt or p-MAPK)	D21 ↔		D21 ↓ SNAT1, ↔ Systems A and L amino acid transport and LPL activity, SNAT2, SNAT4, GLUT1, GLUT3, GLUT9, FATP4, FATP6, LPL	D21 ↑7%	(Gaccioli <i>et al.</i> , 2013)
3-times fat and 5-times sugar diet	Mouse	-D42-D18	D18 ↓ mTORC1 signalling, ↔ Insulin-IGF PI3K (p-AKT, IRS1, PI3K-p85)	D18 ↔			D18 ↔	(Lager <i>et al.</i> , 2014)
4-times fat and 1.3-times sugar	Mouse	-D20-D19	D19 ↑ Insulin/IGF-PI3K (p-IRS1, p-Akt-T308) and mTORC1 signalling, ↔MAPK	D19 ↔		D19 ↑ Systems A and L amino acid transport, SNAT2, LAT1, GLUT1, GLUT3,	D19 ↑18%	(Diaz <i>et al.</i> , 2015; Rosario <i>et al.</i> , 2015; Rosario <i>et al.</i> , 2016)

						FATP6, ↔ SNAT4, LAT2, CD98, FAT/CD36, FATP2, FATP4		
3-times fat and 5-times sugar diet	Mouse	D1-D19	D16 ↑ Igf2, IgfP0, H19, Insulin/IGF-PI3K signalling (PI3K-p110α, p-Akt), ↓ INSR, ↔ mTORC1 or MAPK  D19 ↑ Insulin/IGF-PI3K signalling (PI3K-p110α, p-Akt, p-MAPK), ↔ Igf2, Igf2P0, H19, INSR or mTORC1	D16 ↓11%  D19 ↓8%	D16 ↓Lz FC ↑BT  D19 ↓Lz, MBS, BT, SA and ↓GlyT	D16 ↑ glucose and System A amino acid transport, Glut3, Snat2  D19 ↑ FATP1, ↔ glucose and System A amino acid transport	D16 ↓9%  D19 ↔	(Sferruzzi-Perri <i>et al.</i> , 2013)
50% greater food intake	Sheep	-D60-D135	D70-75 ↓ p-IRS1, p-mTORC1, p-MAPK in the arterial tissues, ↔ INSR, IGF1R  D165 ND	D70-75 ↓22%  D165 ↔	D70-75 ↑ arteriole diameters, ↓ vessel density  D165 ↔	D70-75 ↑ Fatp1, Fatp4, Cd36, Lpl  D165 ↑ GLUT3, FATP1, Fatp4, Cd36, ↔ Lpl	D70-75 ↑20-26%  D165 ↔	(Zhu <i>et al.</i> , 2009; Ma <i>et al.</i> , 2010; Zhu <i>et al.</i> , 2010; Tuersunjiang <i>et al.</i> , 2013)
<b>Hypoxia</b>								
13%	Mouse	D1-D19	D19 ↑ Insulin-IGF	D19 ↑10%	D19 ↑ Maternal	ND	D19 ↓12% weight and	(Matheson <i>et al.</i> ,

			(↑ p-Akt) and mTORC1 signalling		arterial and venous blood space		litter size	2015)
13% hypoxia	Mouse	D11-16	D16 ↓ Igf2, ↔ Igf2P0, altered p-Akt (depending on site phosphorylated)	D16 ↔	D16 ↑ Lz ↑ MBS, trophoblast vol, SA exchange	D16 ↔ System A amino acid amino acid or glucose transport, Gluts and Snats	D16 ↔	{Higgins, 2015 #5541
13% hypoxia	Mouse	D14-19	D19 ↑ Igf2, Igf2P0, altered insulin-IGF signalling (↓ INSR, IGF1R, PI3K-p85α, PI3K-p110α but ↑ p-Akt)	D19 ↔	D19 ↑ FC volume and density, ↓ BT	D19 ↑ glucose transport, Snat1, ↔ System A amino acid amino acid transport	D19 ↓5%	(Higgins <i>et al.</i> , 2015)
12% Hypoxia	Mouse	D14.5-18.5	D18.5 ↓ Igf2r and Igf2, Igf1r in females	D18.5 ↔	D18.5 ↓ Lz blood space, ↑ tissue in females	D18.5 ↓ Glut1, ↑ Snat1 in females, ↔ Glut3	D18.5 ↓6.5%	(Cuffe <i>et al.</i> , 2014)
10% hypoxia	Mouse	D14-19	D19 ↓ Insulin-IGF signalling (↓ INSR, IGF1R, PI3K-p85α, PI3K-p110α and p-Akt), ↔ Igf2, Igf2P0	D19 ↔	D19 ↓ Lz vd, MBS volume, SA exchange, ↑ Jz vd, trophoblast vol and BT	D19 ↓ System A amino acid transport, ↔ glucose transport but altered uterine artery vasoreactivity	D19 ↓21%	(Higgins <i>et al.</i> , 2015; Skeffington <i>et al.</i> , 2015)

<b>Endocrine disruption</b>								
Corticosterone 83µg/g/day	Mouse	D11-D16	D16 ↓ p-Akt, ↔ Igf2, Igf2P0, INSR, IGF1R, mTORC1 signalling	D16 ↓6%	D16 ↓ FC vol and Vd, ↑ MBS and Troph Vd, ↔ SA, BT	D16 ↓ Glut1, Glut3, Snat1, Snat2, ↔ glucose or System A amino acid transport and Snat4	D16 ↓7%	(Vaughan <i>et al.</i> , 2012; Vaughan <i>et al.</i> , 2015)
Corticosterone 81µg/g/day	Mouse	D11-D19	D19 ↓ mTORC1 signalling, ↔ Igf2, Igf2P0, INSR, IGF1R, p- Akt	D19 ↓12%	D19 ↔ FC, MBS, Troph, SA, BT	D19 ↓ glucose and System A amino acid transport, ↑ Snat1, ↔ Glut1, Glut3, Snat2, Snat4	D19 ↓19%	(Vaughan <i>et al.</i> , 2012; Vaughan <i>et al.</i> , 2015)
Dexamethasone 24µg/kg/day	Mouse	D13-D16	D16↓ MAPK1 D18 ↔ MAPK1  D16 and D18 ↔ Igf2	D16 ↓20% female only  D18 ↔	D16↓Jz area female only  D18 ND	D16 and D18 ↔ Glut1, Glut3, Snat1, Snat2, Snat4	D16 ↓20%  D18 ↔	(Cuffe <i>et al.</i> , 2011)
Dexamethasone 24µg/kg/day	Rat	D13-D20	D20 ↓pAkt in Jz	D20 ↓50%		D20 ↓ Prls in Jz, ↑ Prls in Lz	D20 ↓22%	(Ain <i>et al.</i> , 2005)
Diabetes via streptozotocin administration neonatally	Rat		D20 ↑ Igf1, Igf2, Igf2r, IGF1R kinase and autophosphorylation activity, ↔ Igf1r, Insr	D21 ↑22%	D21	D21↑ glycerol and FFA release	D21 ↑13%	(Hauguel-de Mouzon <i>et al.</i> , 1992; Martinez <i>et al.</i> , 2008; White <i>et al.</i> , 2015)

Diabetes via streptozotocin administration 1 week before mating	Rat	-D7-D21	D21↓ Insr, Irs1, Igf2, Igf2r, ↔ Irs2, Igf1r	D21 ↑22%	D21↑ Lz, ↑ lacunae	D21↓ Glut1, ↑ Lpl, ↔ Glut3, Snat2, Snat4, Lat1	D21 ↑5% or ↔	(Cisse <i>et al.</i> , 2013)
Insulin resistance via heterozygous p110α deficiency	Mouse		D16 ↓ PI3K signalling          D19 ↓ PI3K signalling	D16 ↔       D19 ↑15%	D16 ↓ Lz Troph vol, ↓ BT      D19 ↑ Jz vol ↑ SA diffusing capacity	D16 ↓ glucose transfer, Snat1, ↔ System A amino acid transfer, Glut1, Glut3, Snat2, Snat4      D19 ↓ glucose transfer, Glut1, Snat1, Snat2, Prls, ↔ System A amino acid transfer, Glut3, Snat4	D16 ↔       D19 ↔	(Sferruzzi-Perri <i>et al.</i> , 2016)  *Depends on fetal genotype
<b>Other manipulations affecting conceptus growth</b>								
<b>Restriction of utero-placental blood flow</b>								
Uterine ligation	Mouse	D18	D20 ↓ Igf1, Igf2	D20 ↔	D20 ↓ Lz depth, vol,	D20 ↓ Slc5a9,	D20 ↓11%	(Habli <i>et al.</i> , 2013;

					vessel area	Slc7a10, 4F2hc, Lat1, Lat2, Snat2, GLUT1, GLUT8, ↑ Snat1, ↔ GLUT3, GLUT9		Jones <i>et al.</i> , 2013; Jones <i>et al.</i> , 2014)
Uterine ligation	Rat	D17	D20 ↓ Igf2	D20 ↓8%			D20 ↓20%	(Price <i>et al.</i> , 1992)
Uterine ligation	Rat	D18 or D19	D20 ↓ IGF1R, ↔ INSR	D20 ↔ or ↓25%	D20↑ diameter, ↔ Lz vd	D20 ↓ GLUT1, ↔ GLUT3	D20 ↓7% or 27% weight and ↓ litter size	(Das <i>et al.</i> , 1998; Reid <i>et al.</i> , 2002; Wlodek <i>et al.</i> , 2005)
Uterine ligation	Rat	D19	D22 ↓ Igf1, ↔ Igf2, Insr, Igf1r, Igf2r	ND			D22 ↔	(Nusken <i>et al.</i> , 2011)
Uterine ligation	Guinea pig	D30	D55-60 ↔ Igf1, Igf2	D55-60 ↔ or 37%		D55-60 ↓ System A amino acid transfer, ↔ glucose transfer	D55-60 ↓7% or 38%	(Jansson & Persson, 1990; Carter <i>et al.</i> , 2005)
Placental embolism	sheep	D113-120	D131 ↓ IGF1R, ↔ IGF-I	D131 ↓30%			D131 ↓21%	(Bloomfield <i>et al.</i> , 2002a; Shaikh <i>et al.</i> , 2005)
Placental embolism	sheep	D103-109	D131 ↔ Mtor	D131 ↓43%		D131 ↓ Glut1, Slc7a1, Slc7a8, ↔ Glut3, Glut4, Snat4, Slc7a5	D131 ↓20%	(Wali <i>et al.</i> , 2012)



Uterine carunclectomy	sheep	-D70	D130-134 ↑ Igf2, ↔ Igf1, Igf1r,Igf2r	D130-134 ↓ 30-40%	D130-134 altered distribution of placentome types and ↓ placentome number but ↑ individual weight of placentomes, trophoblast and maternal capillary volume and SA of placentomes	D130-134 ↓ Fatp4, ↔ Glut1, Glut3, Glut4, Slc7a1, Slc7a5, Snat1, Snat4, Fatp1, Cd36, Fabp5	D130-134 ↓26%	(Zhang <i>et al.</i> , 2016b)
<b>Hyperthermia</b>	Sheep	D39-D125	D55 ↑ IGF2  D90 ↑ IGF1 , p-mTORC1, ↓ p-Akt, ↔ MAPK  D135 ↑ pAkt, p-MAPK dys-regulated mTORC1 signalling (↑ p- mTORC1 but ↓ p-p70)	D55 ↔  D90 ↓24%  D135 ↓58%		D135 ↑ Slc7a5, Slc7a8, uterine blood flow, trans-placental oxygen diffusion, ↓ branched amino acid and glucose transport,	D55 ↔  D90 ↔  D135 ↓47%	(Thureen <i>et al.</i> , 1992; Ross <i>et al.</i> , 1996; Anderson <i>et al.</i> , 1997; Regnault <i>et al.</i> , 2003; de Vrijer <i>et al.</i> , 2004; Regnault <i>et al.</i> , 2005; de Vrijer <i>et al.</i> , 2006; Regnault <i>et al.</i> , 2007; Arroyo <i>et al.</i> , 2009; Arroyo <i>et al.</i> , 2010)

						↔ utero-placental oxygen uptake		
<b>Alcohol consumption</b>	Rat	-D4-D4	D20 ↓ Lz Igf1, and Lz Igf1r in males, ↔ Igf2  ↑ Jz Igf2, ↔ Jz Igf1, Lz or Jz Igf2r	D20 ↔	D20 ↑ length and width, ↓ Lz and ↑ Jz and ↑ GlyT in females	D20 ↓ Lz Snat2, ↔ Lz Snat1, Snat4, Glut1, Glut3 and ↓ Jz Glut1 in males, ↑ Jz Glut1 in females	D20 ↓ 7%	(Gardebjer <i>et al.</i> , 2014)

1548 Gestational age: mouse ~20 days, rats ~23 days, guinea pigs ~70 days, sheep ~150 days, cows ~283 days, baboons ~183 days.

1549 Abbreviations: BT=barrier thickness, D=day, FATP=fatty acid transport protein, FC=fetal capillaries, GLUT=glucose transporter, GiT- giant trophoblast cells, GlyT- trophoblast glycogen cells,

1550 IGF1/Igf1=insulin-like growth factor-1, IGF2/Igf2=insulin-like growth factor-2, Jz=junctional zone, LAT=cationic amino acid transporter, LPL=lipoprotein lipase, Lz=labyrinthine zone,

1551 MAPK/ERK=mitogen activated kinase, MBS=maternal blood space, mTOR=mechanistic target of rapamycin, p=phosphorylation, PI3K=phosphoinositol 3-kinase, Prl=prolactin-related hormone,

1552 SA=surface area, SNAT/Slc38a= Sodium-coupled neutral amino acid transporter, UN=undernutrition; vol=volume, vd=volume density.

1553 **Search terms used:** placenta, fetus, insulin-like growth factor, IGF, nutrient restriction, undernutrition, low protein diet, high sugar, high fat, obesogenic, IUGR, PI, hypoxia, uterine ligation,

1554 corticosterone, dexamethasone carunclectomy, heat stress and/or diabetes.

1555

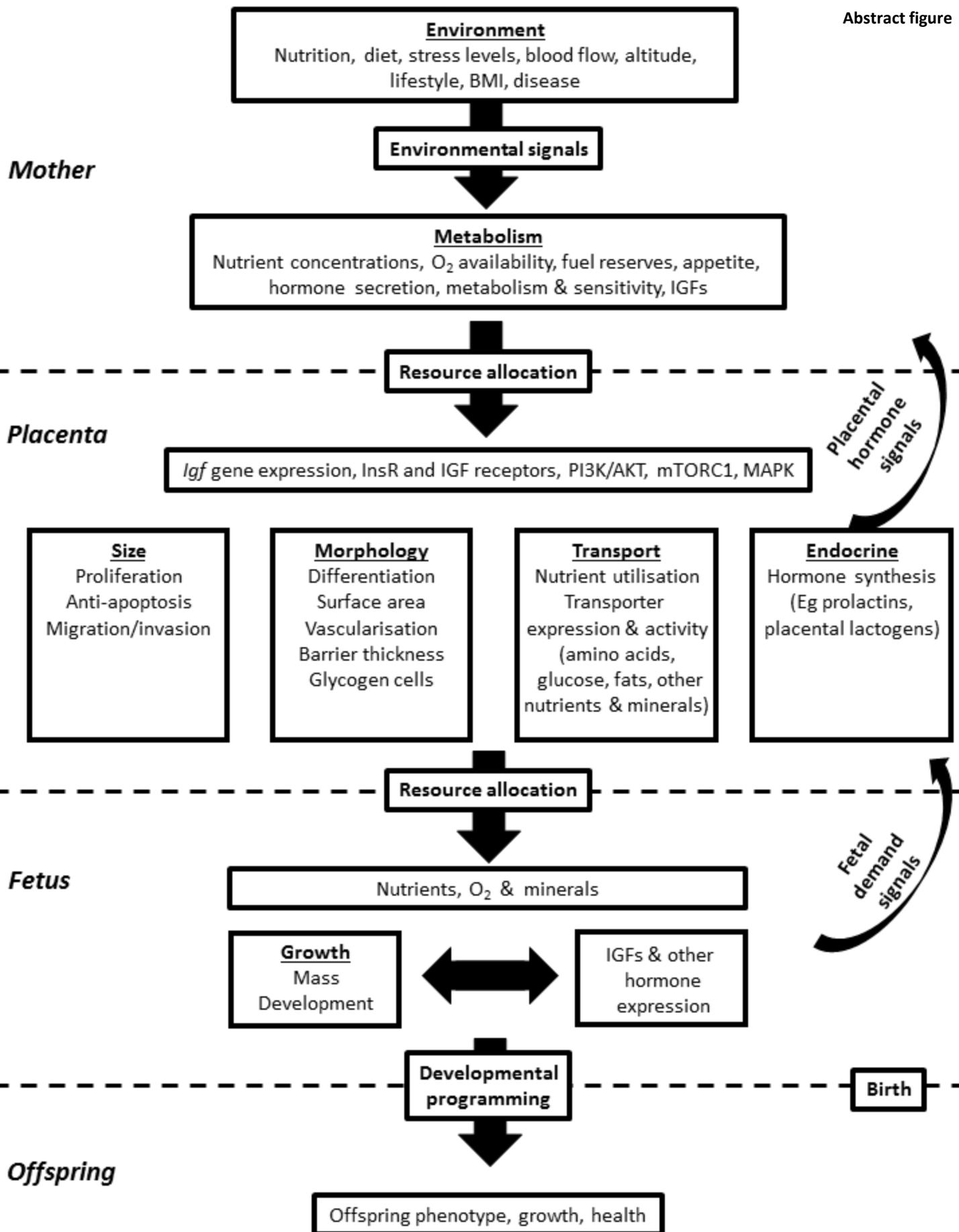


Figure 1

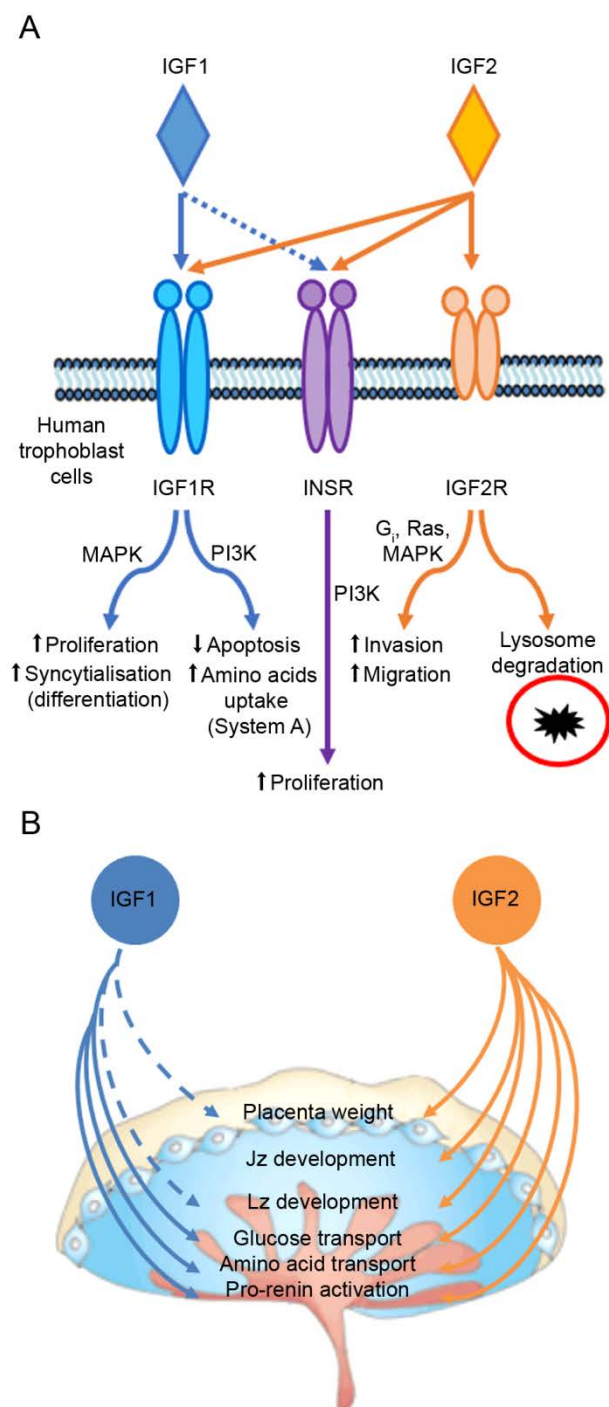


Figure 2

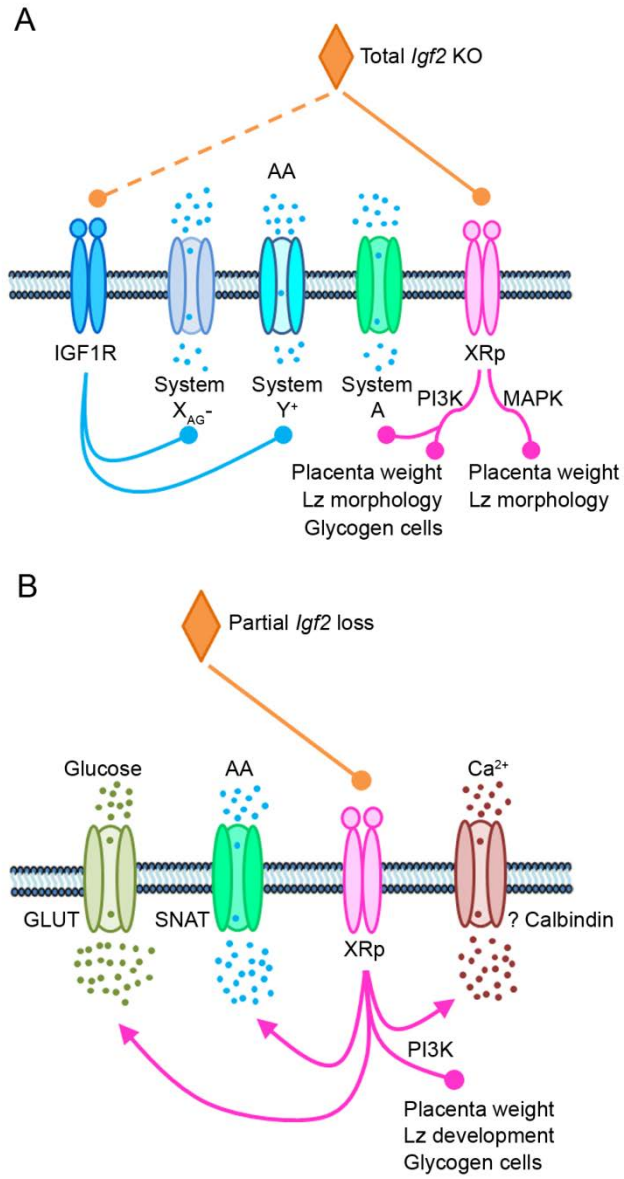
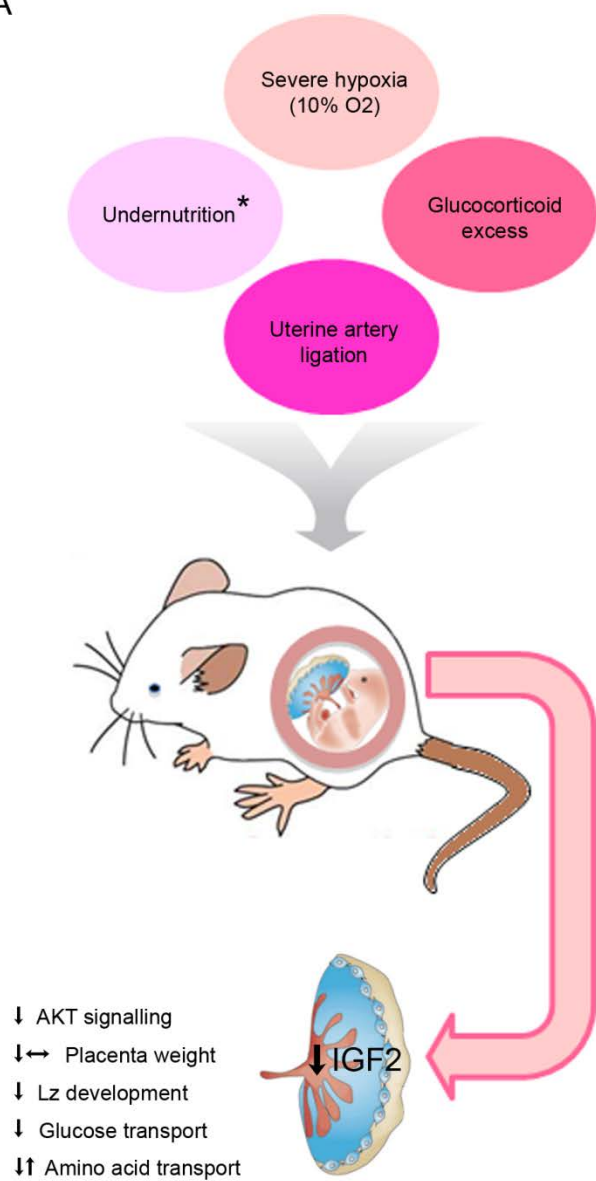


Figure 3

A



B

